



SEQUENCE LISTING

<110> HIRANO, SEIKO
KIMURA, EIICHIRO
OSUMI, TSUYOSHI
MATSUI, KAZUHIKO
KAWAHARA, YOSHIO
NONAKA, GEN
MATSUZAKI, YUMI
AKIYOSHI, NAOKI
NAKAMURA, KANAE
KURAHASHI, OSAMU
NAKAMATSU, TSUYOSHI
SUGIMOTO, SHINICHI

<120> GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC
PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

<130> 221519US0PCT

<140> 10/089,057

<141> 2002-04-03

<150> PCT/JP00/06913

<151> 2000-10-04

<150> JP 11-282716

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<151> 1999-11-01

<150> JP 2000-120687

<151> 2000-04-21

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<170> PatentIn version 3.1

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<213> Corynebacterium thermoaminogenes

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Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys						
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Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly						
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Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp						
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cag ctc gca cgc cac cgc acc acc gcg ttc ggc ctg ggc aac aag cga						596
Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg						
	75		80		85	
ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc						644
Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg						
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Gly	Ala	Thr	Thr	His	Met	Val	Thr	Ala	Gly	Asn	Ser	His	Tyr	Thr	Val	
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Leu	Pro	Ser	Asn	Asn	Arg	Ser	Tyr	Ala	Pro	Val	Glu	Glu	Phe	Asp	Glu	
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Glu	Asp	Gly	Gly	Ile	Ala	Glu	Asn	Ile	Thr	Ala	Asp	Asp	Leu	Lys	Leu	
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Ser	Val	Gly	Phe	Val	Ala	Asn	Gln	Pro	Thr	Gln	Phe	Ala	Gly	Cys	Leu	
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<213> Corynebacterium thermoaminogenes

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Tyr	Arg	Lys	Glu	Leu	Met	Ala	Ala	Asp	Ala	Lys	Gly	Leu	Asp	Thr	Val
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<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

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Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val						
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Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu						
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Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr						

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Glu	Gly	Val	Val	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	Phe	Tyr	Arg	Asn	
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acc	cag	gca	tcc	ggt	gtc	atc	cca	cag	atc	tcc	ctc	atc	atg	ggt	gcc	945
Thr	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Leu	Ile	Met	Gly	Ala	
		165					170					175				
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Cys	Ala	Gly	Gly	His	Val	Tyr	Ser	Pro	Ala	Leu	Thr	Asp	Phe	Ile	Ile	
	180					185				190						
atg	gtg	gac	aag	acc	tcc	aag	atg	ttc	atc	acc	ggc	ccc	gac	gtg	atc	1041
Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Ile	Thr	Gly	Pro	Asp	Val	Ile	
					200					205					210	
aag	acc	gtc	acc	ggc	gag	gag	gtc	acc	cag	gag	gaa	ctg	ggt	ggt	gcc	1089
Lys	Thr	Val	Thr	Gly	Glu	Glu	Val	Thr	Gln	Glu	Glu	Leu	Gly	Gly	Ala	
				215					220					225		
tac	acc	cac	atg	gcc	cag	tcc	ggc	acc	tcg	cac	tac	acc	gca	gcc	gat	1137
Tyr	Thr	His	Met	Ala	Gln	Ser	Gly	Thr	Ser	His	Tyr	Thr	Ala	Ala	Asp	
			230					235					240			
gac	tcc	gat	gcc	ctc	gac	tgg	gtc	cgt	gag	ctg	gtc	agc	tac	ctg	ccg	1185
Asp	Ser	Asp	Ala	Leu	Asp	Trp	Val	Arg	Glu	Leu	Val	Ser	Tyr	Leu	Pro	
		245					250					255				
tcc	aac	aac	cgt	gcg	gag	acc	cca	cgc	cag	gac	gcc	gac	atc	atg	gtg	1233
Ser	Asn	Asn	Arg	Ala	Glu	Thr	Pro	Arg	Gln	Asp	Ala	Asp	Ile	Met	Val	
	260					265				270						
ggc	tcc	atc	aag	gag	aac	atc	acc	gag	acc	gac	ctc	gaa	ctc	gac	acc	1281
Gly	Ser	Ile	Lys	Glu	Asn	Ile	Thr	Glu	Thr	Asp	Leu	Glu	Leu	Asp	Thr	
					280					285					290	
ctg	atc	ccg	gat	tcc	ccg	aac	cag	ccg	tac	gac	atg	aag	gac	gtc	atc	1329
Leu	Ile	Pro	Asp	Ser	Pro	Asn	Gln	Pro	Tyr	Asp	Met	Lys	Asp	Val	Ile	
				295					300					305		
acc	cgc	atc	gtc	gat	gat	gcc	gag	ttc	ttc	gag	atc	cag	gag	ggt	tac	1377
Thr	Arg	Ile	Val	Asp	Asp	Ala	Glu	Phe	Phe	Glu	Ile	Gln	Glu	Gly	Tyr	
			310					315					320			
gcc	gag	aac	atc	atc	tgc	ggt	ttc	gcc	cgc	gtc	gag	ggt	cgt	gcc	gtg	1425
Ala	Glu	Asn	Ile	Ile	Cys	Gly	Phe	Ala	Arg	Val	Glu	Gly	Arg	Ala	Val	
		325				330						335				
ggt	atc	gtg	gcc	aac	cag	ccg	atg	cag	ttc	gcc	ggc	tgc	ctg	gac	atc	1473
Gly	Ile	Val	Ala	Asn	Gln	Pro	Met	Gln	Phe	Ala	Gly	Cys	Leu	Asp	Ile	
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aag	gca	tcc	gag	aag	gcc	gcc	cgc	ttc	atc	cgc	acc	tgt	gac	gcc	ttc	1521
Lys	Ala	Ser	Glu	Lys	Ala	Ala	Arg	Phe	Ile	Arg	Thr	Cys	Asp	Ala	Phe	
					360					365					370	
aac	atc	ccg	atc	atc	gag	ctt	gtc	gac	gtc	cca	ggc	ttc	ctc	ccg	ggc	1569
Asn	Ile	Pro	Ile	Ile	Glu	Leu	Val	Asp	Val	Pro	Gly	Phe	Leu	Pro	Gly	
				375					380					385		
acc	aac	cag	gag	ttc	gac	ggc	atc	atc	cgt	cgc	ggc	gcg	aag	ctg	ctc	1617
Thr	Asn	Gln	Glu	Phe	Asp	Gly	Ile	Ile	Arg	Arg	Gly	Ala	Lys	Leu	Leu	

			390					395					400				
tac	gcc	tac	gcc	gag	gcc	acc	gtc	ggc	aag	atc	acc	gtg	atc	acc	cgc		1665
Tyr	Ala	Tyr	Ala	Glu	Ala	Thr	Val	Gly	Lys	Ile	Thr	Val	Ile	Thr	Arg		
		405					410					415					
aag	tcc	tac	ggc	ggt	gcc	tac	tgc	gtg	atg	ggc	tcc	aag	gac	atg	ggt		1713
Lys	Ser	Tyr	Gly	Gly	Ala	Tyr	Cys	Val	Met	Gly	Ser	Lys	Asp	Met	Gly		
	420					425					430						
gcg	gac	ctc	gtc	ttc	gca	tgg	ccc	acc	gcg	cag	atc	gcc	gtc	atg	ggt		1761
Ala	Asp	Leu	Val	Phe	Ala	Trp	Pro	Thr	Ala	Gln	Ile	Ala	Val	Met	Gly		
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Ala	Ser	Gly	Ala	Val	Gly	Phe	Ile	Tyr	Arg	Lys	Glu	Leu	Lys	Gln	Ala		
				455					460					465			
gca	gcg	gcc	ggc	gag	gat	gtc	acc	gcg	ctg	atg	aag	aag	tac	gag	cag		1857
Ala	Ala	Ala	Gly	Glu	Asp	Val	Thr	Ala	Leu	Met	Lys	Lys	Tyr	Glu	Gln		
			470					475					480				
gag	tac	gag	gag	acc	ctg	gtc	aac	ccg	tac	atg	gct	gca	gag	cgt	ggc		1905
Glu	Tyr	Glu	Glu	Thr	Leu	Val	Asn	Pro	Tyr	Met	Ala	Ala	Glu	Arg	Gly		
		485					490					495					
tac	gtc	gac	gcc	gtc	atc	cca	cca	tcc	gag	acc	cgt	ggc	cag	atc	atc		1953
Tyr	Val	Asp	Ala	Val	Ile	Pro	Pro	Ser	Glu	Thr	Arg	Gly	Gln	Ile	Ile		
	500					505					510						
gag	ggt	ctg	cgt	ctg	ctc	gac	cgc	aag	gtg	gtc	aac	gtc	ccg	gcc	aag		2001
Glu	Gly	Leu	Arg	Leu	Leu	Asp	Arg	Lys	Val	Val	Asn	Val	Pro	Ala	Lys		
515					520					525					530		
aag	cac	ggt	aac	atc	ccg	ctg	taaaccgtct tcccctccgg caccacgccg										2052
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<210> 8

<211> 537

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 8

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Gln	Ala	Ser	Val	Glu	Lys	Val	His	Glu	Ala	Gly	Lys	Lys	Thr	Ala	Arg	
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Glu	Arg	Ile	Glu	Tyr	Leu	Leu	Asp	Glu	Gly	Ser	Phe	Val	Glu	Val	Asp	
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Ala	Leu	Ala	Arg	His	Arg	Ser	Lys	Asn	Phe	Gly	Leu	Asp	Ser	Lys	Arg	
65				70					75					80		
Pro	Val	Thr	Asp	Gly	Val	Val	Thr	Gly	Tyr	Gly	Thr	Ile	Asp	Gly	Arg	
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Lys	Val	Cys	Val	Phe	Ser	Gln	Asp	Gly	Ala	Ile	Phe	Gly	Gly	Ala	Leu	
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Gly	Glu	Val	Tyr	Gly	Glu	Lys	Ile	Val	Lys	Ile	Met	Asp	Leu	Ala	Ile	

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Lys	Thr	Gly	Val	Pro	Leu	Ile	Gly	Ile	Asn	Glu	Gly	Ala	Gly	Ala	Arg
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Ile	Gln	Glu	Gly	Val	Val	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	Phe	Tyr
145					150					155					160
Arg	Asn	Thr	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Leu	Ile	Met
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Gly	Ala	Cys	Ala	Gly	Gly	His	Val	Tyr	Ser	Pro	Ala	Leu	Thr	Asp	Phe
			180					185						190	
Ile	Ile	Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Ile	Thr	Gly	Pro	Asp
		195					200					205			
Val	Ile	Lys	Thr	Val	Thr	Gly	Glu	Glu	Val	Thr	Gln	Glu	Glu	Leu	Gly
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Gly	Ala	Tyr	Thr	His	Met	Ala	Gln	Ser	Gly	Thr	Ser	His	Tyr	Thr	Ala
225					230					235					240
Ala	Asp	Asp	Ser	Asp	Ala	Leu	Asp	Trp	Val	Arg	Glu	Leu	Val	Ser	Tyr
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Leu	Pro	Ser	Asn	Asn	Arg	Ala	Glu	Thr	Pro	Arg	Gln	Asp	Ala	Asp	Ile
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Met	Val	Gly	Ser	Ile	Lys	Glu	Asn	Ile	Thr	Glu	Thr	Asp	Leu	Glu	Leu
		275					280					285			
Asp	Thr	Leu	Ile	Pro	Asp	Ser	Pro	Asn	Gln	Pro	Tyr	Asp	Met	Lys	Asp
	290					295					300				
Val	Ile	Thr	Arg	Ile	Val	Asp	Asp	Ala	Glu	Phe	Phe	Glu	Ile	Gln	Glu
305					310					315					320
Gly	Tyr	Ala	Glu	Asn	Ile	Ile	Cys	Gly	Phe	Ala	Arg	Val	Glu	Gly	Arg
				325				330						335	
Ala	Val	Gly	Ile	Val	Ala	Asn	Gln	Pro	Met	Gln	Phe	Ala	Gly	Cys	Leu
			340				345						350		
Asp	Ile	Lys	Ala	Ser	Glu	Lys	Ala	Ala	Arg	Phe	Ile	Arg	Thr	Cys	Asp
		355					360					365			
Ala	Phe	Asn	Ile	Pro	Ile	Ile	Glu	Leu	Val	Asp	Val	Pro	Gly	Phe	Leu
	370					375					380				
Pro	Gly	Thr	Asn	Gln	Glu	Phe	Asp	Gly	Ile	Ile	Arg	Arg	Gly	Ala	Lys
385					390					395					400
Leu	Leu	Tyr	Ala	Tyr	Ala	Glu	Ala	Thr	Val	Gly	Lys	Ile	Thr	Val	Ile
				405					410					415	
Thr	Arg	Lys	Ser	Tyr	Gly	Gly	Ala	Tyr	Cys	Val	Met	Gly	Ser	Lys	Asp
			420					425					430		
Met	Gly	Ala	Asp	Leu	Val	Phe	Ala	Trp	Pro	Thr	Ala	Gln	Ile	Ala	Val
		435					440					445			
Met	Gly	Ala	Ser	Gly	Ala	Val	Gly	Phe	Ile	Tyr	Arg	Lys	Glu	Leu	Lys
		450				455					460				
Gln	Ala	Ala	Ala	Ala	Gly	Glu	Asp	Val	Thr	Ala	Leu	Met	Lys	Lys	Tyr
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Glu	Gln	Glu	Tyr	Glu	Glu	Thr	Leu	Val	Asn	Pro	Tyr	Met	Ala	Ala	Glu
				485					490					495	
Arg	Gly	Tyr	Val	Asp	Ala	Val	Ile	Pro	Pro	Ser	Glu	Thr	Arg	Gly	Gln
			500					505					510		
Ile	Ile	Glu	Gly	Leu	Arg	Leu	Leu	Asp	Arg	Lys	Val	Val	Asn	Val	Pro
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<211> 1643
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (326)..(1363)

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ctttgagttt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180
ctgggggtggc ggacaccatg tccgttcggg cgttgccccg acgggggaaa atcgcaggca 240
gatgtgtccg atgtgggata aacccaccgg ttcggggcgtg tcttcgggat caatggcaca 300
gcattaaccg tgtgggggggt ttaat atg gga gcc atg cga att gcc act ctc 352
Met Gly Ala Met Arg Ile Ala Thr Leu
1 5
acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc 400
Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile
10 15 20 25
gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag 448
Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln
30 35 40
gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac 496
Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp
45 50 55
gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc 544
Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly
60 65 70
acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc 592
Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val
75 80 85
aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt 640
Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly
90 95 100 105
ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc 688
Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile
110 115 120
ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg 736
Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr
125 130 135
gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc 784
Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala
140 145 150
atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc 832
Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile
155 160 165

gtc	gag	gtc	atg	ggc	cgc	cac	gtc	ggg	tgg	atc	gca	ctg	cat	gcc	ggc	880
Val	Glu	Val	Met	Gly	Arg	His	Val	Gly	Trp	Ile	Ala	Leu	His	Ala	Gly	
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Met	Ala	Gly	Gly	Ala	His	Tyr	Thr	Val	Ile	Pro	Glu	Val	Pro	Phe	Asp	
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Ile	Ser	Glu	Ile	Cys	Lys	Arg	Met	Glu	Arg	Arg	Phe	Gln	Met	Gly	Glu	
			205					210					215			
aag	tac	ggc	atc	atc	gtc	gtc	gcg	gag	ggg	gcc	ctg	ccc	aag	gag	gga	1024
Lys	Tyr	Gly	Ile	Ile	Val	Val	Ala	Glu	Gly	Ala	Leu	Pro	Lys	Glu	Gly	
		220					225					230				
acc	atg	gag	ctg	cgt	gag	ggg	gag	gtg	gat	cag	ttc	ggg	cac	aag	acc	1072
Thr	Met	Glu	Leu	Arg	Glu	Gly	Glu	Val	Asp	Gln	Phe	Gly	His	Lys	Thr	
	235				240					245						
ttc	acc	ggc	atc	ggc	cag	cag	atc	gcc	gac	gag	gtg	cac	agg	cgt	ctg	1120
Phe	Thr	Gly	Ile	Gly	Gln	Gln	Ile	Ala	Asp	Glu	Val	His	Arg	Arg	Leu	
250				255						260					265	
ggg	cat	gat	gtc	cgc	acc	acg	gtc	ctg	ggc	cat	atc	cag	cgt	ggg	ggc	1168
Gly	His	Asp	Val	Arg	Thr	Thr	Val	Leu	Gly	His	Ile	Gln	Arg	Gly	Gly	
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acc	ccc	acc	gcc	ttc	gac	cgt	gtc	ctg	gcc	acc	cgg	tac	ggg	gtc	cgc	1216
Thr	Pro	Thr	Ala	Phe	Asp	Arg	Val	Leu	Ala	Thr	Arg	Tyr	Gly	Val	Arg	
			285					290					295			
gcc	gcg	cgt	gcc	tgc	cac	gag	ggg	cag	ttc	aac	acc	gtg	gtc	gcg	ctc	1264
Ala	Ala	Arg	Ala	Cys	His	Glu	Gly	Gln	Phe	Asn	Thr	Val	Val	Ala	Leu	
		300					305					310				
aag	ggg	gag	cgc	atc	cgg	atg	atc	tcc	ttc	gat	gag	gcc	gtg	ggc	acc	1312
Lys	Gly	Glu	Arg	Ile	Arg	Met	Ile	Ser	Phe	Asp	Glu	Ala	Val	Gly	Thr	
	315					320					325					
ctg	aag	aag	gtg	ccg	atg	gaa	cgc	tgg	gtg	acc	gcc	cag	gct	atg	ttc	1360
Leu	Lys	Lys	Val	Pro	Met	Glu	Arg	Trp	Val	Thr	Ala	Gln	Ala	Met	Phe	
330				335						340					345	
ggg	tagtcaggcc	gcattcccgg	ttccgcgccc	gcggggccgg	gtttttttcat											1413
Gly																
gccccggaac	acatcggtat	gaaatcgtga	tatgcattac	ttgacgggga	agtgggggat											1473
ccgtcacctc	gcgttgtcca	actacagccc	gcagcgcctg	cgggaattct	tcgagcaatc											1533
cgccgattcc	ccggcccgtc	ccgtcgccgt	ccaaccgcag	tacaatctgc	tggcccgcgg											1593
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 <211> 346
 <212> PRT
 <213> Corynebacterium thermoaminogenes

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 20 25 30
 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu

		35					40					45			
Ala	Asp	Arg	Arg	Val	Gln	Leu	Tyr	Asp	Asp	Glu	Asp	Ile	Asp	Arg	Ile
	50					55					60				
Leu	Leu	Arg	Gly	Gly	Thr	Ile	Leu	Gly	Thr	Gly	Arg	Leu	His	Pro	Asp
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Lys	Phe	Arg	Ala	Gly	Ile	Asp	Gln	Val	Lys	Ala	Asn	Leu	Ala	Asp	Ala
				85					90					95	
Gly	Ile	Asp	Ala	Leu	Ile	Pro	Ile	Gly	Gly	Glu	Gly	Thr	Leu	Lys	Gly
			100					105					110		
Ala	Lys	Trp	Leu	Ala	Asp	Asn	Gly	Ile	Pro	Val	Val	Gly	Val	Pro	Lys
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Thr	Ile	Asp	Asn	Asp	Val	Asn	Gly	Thr	Asp	Phe	Thr	Phe	Gly	Phe	Asp
	130					135					140				
Ser	Ala	Val	Ser	Val	Ala	Thr	Asp	Ala	Ile	Asp	Arg	Leu	His	Thr	Thr
145					150					155					160
Ala	Glu	Ser	His	Asn	Arg	Val	Met	Ile	Val	Glu	Val	Met	Gly	Arg	His
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Val	Gly	Trp	Ile	Ala	Leu	His	Ala	Gly	Met	Ala	Gly	Gly	Ala	His	Tyr
			180					185					190		
Thr	Val	Ile	Pro	Glu	Val	Pro	Phe	Asp	Ile	Ser	Glu	Ile	Cys	Lys	Arg
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Ala	Glu	Gly	Ala	Leu	Pro	Lys	Glu	Gly	Thr	Met	Glu	Leu	Arg	Glu	Gly
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Glu	Val	Asp	Gln	Phe	Gly	His	Lys	Thr	Phe	Thr	Gly	Ile	Gly	Gln	Gln
			245						250					255	
Ile	Ala	Asp	Glu	Val	His	Arg	Arg	Leu	Gly	His	Asp	Val	Arg	Thr	Thr
			260					265					270		
Val	Leu	Gly	His	Ile	Gln	Arg	Gly	Gly	Thr	Pro	Thr	Ala	Phe	Asp	Arg
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Val	Leu	Ala	Thr	Arg	Tyr	Gly	Val	Arg	Ala	Ala	Arg	Ala	Cys	His	Glu
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Gly	Gln	Phe	Asn	Thr	Val	Val	Ala	Leu	Lys	Gly	Glu	Arg	Ile	Arg	Met
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Ile	Ser	Phe	Asp	Glu	Ala	Val	Gly	Thr	Leu	Lys	Lys	Val	Pro	Met	Glu
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<211> 498

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (1)..(498)

<400> 11

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Trp	Ala	His	Thr 20	Thr	Thr	Pro	Leu	Thr 25	Gly	Pro	Gln	Arg	Leu 30	Gln	Trp	
acg	cac	ctg	ccc	gat	gct	ctt	tac	ccg	gat	gta	tcc	tat	gac	ctg	gat	144
Thr	His	Leu 35	Pro	Asp	Ala	Leu	Tyr 40	Pro	Asp	Val	Ser	Tyr 45	Asp	Leu	Asp	
gga	tgc	tat	tcc	ggc	gga	gcc	gta	ttt	tct	gac	ggc	acg	ctt	aaa	ctt	192
Gly	Cys 50	Tyr	Ser	Gly	Gly	Ala 55	Val	Phe	Ser	Asp	Gly 60	Thr	Leu	Lys	Leu	
ttc	tac	acc	ggc	aac	cga	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	240
Phe 65	Tyr	Thr	Gly	Asn 70	Arg	Lys	Ile	Asp	Gly	Lys 75	Arg	Arg	Ala	Thr 80	Gln	
aac	ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	288
Asn	Leu	Val	Glu 85	Val	Glu	Asp	Pro	Thr 90	Gly	Leu	Met	Gly	Gly	Ile 95	His	
cgc	cgc	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggg	ttt	336
Arg	Arg	Ser 100	Pro	Lys	Asn	Pro	Leu 105	Ile	Asp	Gly	Pro	Ala 110	Ser	Gly	Phe	
acg	ccc	cac	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggg	gat	ggg	tgg	384
Thr	Pro 115	His	Tyr	Arg	Asp	Pro	Met 120	Ile	Ser	Pro	Asp 125	Gly	Asp	Gly	Trp	
aag	atg	gtt	ctt	ggg	gct	cag	cgc	gaa	aac	ctc	acc	ggg	gca	gcg	gtt	432
Lys 130	Met	Val	Leu	Gly	Ala	Gln 135	Arg	Glu	Asn	Leu 140	Thr	Gly	Ala	Ala	Val	
cta	tac	cgc	tcg	gca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggg	gaa	atc	480
Leu 145	Tyr	Arg	Ser	Ala 150	Asp	Leu	Glu	Asn	Trp 155	Glu	Phe	Ser	Gly	Glu 160	Ile	
acc	ttt	gac	ctc	agc	gac											498
Thr	Phe	Asp	Leu	Ser 165	Asp											

<210> 12

<211> 166

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 12

Tyr 1	Tyr	Gln	His	Asp 5	Pro	Gly	Phe	Pro	Phe 10	Ala	Pro	Lys	Arg	Thr 15	Gly	
Trp	Ala	His	Thr 20	Thr	Thr	Pro	Leu	Thr 25	Gly	Pro	Gln	Arg	Leu 30	Gln	Trp	
Thr	His	Leu 35	Pro	Asp	Ala	Leu	Tyr 40	Pro	Asp	Val	Ser	Tyr 45	Asp	Leu	Asp	
Gly	Cys 50	Tyr	Ser	Gly	Gly	Ala 55	Val	Phe	Ser	Asp	Gly 60	Thr	Leu	Lys	Leu	
Phe 65	Tyr	Thr	Gly	Asn 70	Arg	Lys	Ile	Asp	Gly	Lys 75	Arg	Arg	Ala	Thr 80	Gln	
Asn	Leu	Val	Glu 85	Val	Glu	Asp	Pro	Thr 90	Gly	Leu	Met	Gly	Gly	Ile 95	His	

Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	
			100					105					110			
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	
		115					120					125				
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	
	130					135					140					
Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	
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Thr	Phe	Asp	Leu	Ser	Asp											
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<210> 13

<211> 479

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<400> 13

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Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	
1				5					10					15		
tgg	gct	cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	96
Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	
			20				25				30					
acg	cac	ctg	ccc	gac	gct	ctt	tac	ccg	gat	gca	tcc	tat	gac	ctg	gat	144
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp	
		35				40					45					
gga	tgc	tat	tcc	ggt	gga	gcc	gta	ttt	act	gac	ggc	aca	ctt	aaa	ctt	192
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu	
	50				55						60					
ttc	tac	acc	ggc	aac	cta	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	240
Phe	Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
65				70					75						80	
aac	ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	288
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
			85					90						95		
cgc	cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggt	ttc	336
Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	
			100					105					110			
aca	ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggt	gat	ggt	tgg	384
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	
		115					120					125				
aaa	atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggt	gca	gcg	gtt	432
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	
	130					135					140					
cta	tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggt	gaa	at	479
Leu	Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu		
145					150					155						

<210> 14
 <211> 159
 <212> PRT
 <213> Corynebacterium thermoaminogenes

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 Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
 20 25 30
 Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
 35 40 45
 Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
 50 55 60
 Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
 65 70 75 80
 Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
 85 90 95
 Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
 100 105 110
 Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
 115 120 125
 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
 145 150 155

<210> 15
 <211> 490
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<400> 15
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 aatgcattgg ggacacgcac gtagtaaaga tttagttcat tgggaaacat taccgattgc 120
 tttagaacct ggagatgaag aagaaaaaatg gttgtttctc tggtagacagt atagtcaaag 180
 atgataagtt gtatttatatt tatacaggtc accattatta taatgacgat gatcccgatc 240
 attttttgga aaatcaaaaat atggccttata gtgaagatgg cattcathtt caaaaatata 300
 aacaaaatgc aatcattcct accccacctg aagataatac acatcacttc agagatccaa 360
 aggtatggga acatccatgg cttattatta catgatagta ggtagtcaaa atgatagaga 420
 attaggacgt attatcttat atcgttctga ggatttatag aggggaattc tggtcctgag 480
 atcaatccaa 490

<210> 16
 <211> 4254
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS

<222> (637) .. (1362)

<220>

<221> CDS

<222> (1434) .. (2315)

<220>

<221> CDS

<222> (2432) .. (3115)

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<222> (3235) .. (4065)

<400> 16

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cctcctcgag	cagaccggag	agacgctcgg	aatcgtggac	gttcattctg	cagccgaagg	180
tacgcacctc	ataggtgcgg	gcagtgggtg	cctcccgggt	cccccgcgcc	gggaggggtg	240
cggcgggggt	gtccgggtgg	gatggatggg	tgttcattct	gtgggtatca	atctgctgcg	300
tcacggggag	taattgtatc	ggccgcgggc	accctgacat	aaacgtccga	tccagaggaa	360
cgcaaccccc	tggagtgtcg	cagccatgca	ggttgggcaa	caccgtaacg	gaacctagca	420
gagtggtagg	attgacttca	cattctttac	ctattgagct	attgataaaa	tccggggcga	480
aatggaaatc	acccccacaa	atcaccccaa	ctgacctgtg	gaaagggcga	gaaatccagg	540
gaaattcatt	tcaaaatgga	ctcaatcaca	ggatttacct	cacatgacct	aacattcctt	600
tatgctatcc	ccatgacgca	gaccacaaat	cacccg atg	atc aag atg acg ggg		654
			Met	Ile Lys Met Thr Gly		
			1	5		
gtg cag aag ttc ttc gat gac ttc cag gcc ctg acc gat atc aat ctt						702
Val Gln Lys Phe Phe Asp Asp Phe Gln Ala Leu Thr Asp Ile Asn Leu						
	10		15		20	
gag gtc ccc gcg gga cag gtc gtt gtt gtt ctc ggc ccg tcc ggt tcc						750
Glu Val Pro Ala Gly Gln Val Val Val Leu Gly Pro Ser Gly Ser						
	25		30		35	
gga aag tcg acg ctg tgc cgc acc atc aac cgc ctc gaa acc atc gag						798
Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg Leu Glu Thr Ile Glu						
	40		45		50	
gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag						846
Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys						
	55		60		65	70
gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc						894
Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe						
	75		80		85	
aac ctc ttc ccc cac ctc acc atc aag gac aat gtc acc ctc ggc ccg						942
Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro						
	90		95		100	
atg aag gtc cgg aag atg aag aag tcc gag gcc aat gag gtg gcc atg						990
Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met						
	105		110		115	
aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg						1038
Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro						

120	125	130	
gca cag ctc tcg ggc ggg cag cag cag cgc gtg gcc atc gcc cgc gca			1086
Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala			
135	140	145	150
ctg gcg atg aac ccc aag atc atg ctt ttc gac gaa cca acc tcc gcc			1134
Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp Glu Pro Thr Ser Ala			
	155	160	165
ctc gac ccc gag atg gtc aac gag gtt ctg gac gtc atg gcg agt ctg			1182
Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp Val Met Ala Ser Leu			
	170	175	180
gcc aag gaa ggc atg acc atg gtg tgt gtc acc cac gag atg ggt ttc			1230
Ala Lys Glu Gly Met Thr Met Val Cys Val Thr His Glu Met Gly Phe			
	185	190	195
gca cgc agg gcc gca gac cgt gtg ctg ttc atg tct gac ggc gcc atc			1278
Ala Arg Arg Ala Ala Asp Arg Val Leu Phe Met Ser Asp Gly Ala Ile			
	200	205	210
gtc gag gac tcc gac ccg gag acc ttc ttc acc aat cca caa acc gac			1326
Val Glu Asp Ser Asp Pro Glu Thr Phe Phe Thr Asn Pro Gln Thr Asp			
	215	220	225
cgg gcg aag gat ttc ctg ggc aag atc ctc gcc cac tgacctcccc			1372
Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala His			
	235	240	
tcactctgtg tccaactccc ccgctggcca aaatcagcga ccatgaccaa caggagcatc			1432
a atg tcg cac aaa cgc atg ttc acc cgt ctc gcc gca gcc acc agc gca			1481
Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala			
	245	250	255
gct gtt ctc gcc ggc atc acc ctc acc gcc tgt ggt gat tcc gag ggt			1529
Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly			
	260	265	270
ggt gac ggt ctg ctc gcc gcc atc gaa aat ggc aat gtc acc atc ggc			1577
Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly			
	275	280	285
acc aag tac gat cag ccg ggt ctg gga ctg cgt aac ccg gac aat tcc			1625
Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser			
	295	300	305
atg agc gga ctg gat gtc gac gtc gcg cag tac gtg gtc aac tcc atc			1673
Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile			
	310	315	320
gcc gat gac aac ggt tgg gat cac ccc acc gtg gaa tgg cgc gag acc			1721
Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr			
	325	330	335
ccc tcc gcc cag cgc gag acc ctc atc cag aac ggt gag gtg gat atg			1769
Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met			
	340	345	350
atc gcc gca acc tac tcc atc aac ccc gga cgc tcc gaa tcg gtg aac			1817
Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn			
	355	360	365
ttc ggt gga cca tac ctc ctc acc cac cag gcc ctc ctg gtc cgc gag			1865
Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu			
	375	380	385
gac gat gac cgc atc cag acc ctc gag gac ctc gat gac ggc ctg atc			1913

Asp	Asp	Asp	Arg	Ile	Gln	Thr	Leu	Glu	Asp	Leu	Asp	Asp	Gly	Leu	Ile	
			390					395					400			
ctg	tgt	tcc	ggt	acc	gga	tcc	acc	ccc	gcc	cag	aag	gtc	aag	gat	gtc	1961
Leu	Cys	Ser	Val	Thr	Gly	Ser	Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val	
		405					410					415				
ctc	ccc	ggc	gtc	cag	ctg	cag	gaa	tac	gac	acc	tac	tcc	tcc	tgt	gtg	2009
Leu	Pro	Gly	Val	Gln	Leu	Gln	Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val	
	420					425					430					
gag	gca	ctg	agc	cag	ggc	aac	gtc	gat	gca	atg	acc	acc	gac	gcc	acc	2057
Glu	Ala	Leu	Ser	Gln	Gly	Asn	Val	Asp	Ala	Met	Thr	Thr	Asp	Ala	Thr	
435					440					445					450	
atc	ctc	ttc	ggc	tac	gcg	cag	cag	cgc	gaa	ggg	gaa	ttc	cgc	gtc	gtg	2105
Ile	Leu	Phe	Gly	Tyr	Ala	Gln	Gln	Arg	Glu	Gly	Glu	Phe	Arg	Val	Val	
			455					460						465		
gag	atg	gaa	cag	gac	ggc	gag	ccg	ttc	acc	aat	gag	tac	tac	ggc	atc	2153
Glu	Met	Glu	Gln	Asp	Gly	Glu	Pro	Phe	Thr	Asn	Glu	Tyr	Tyr	Gly	Ile	
			470					475					480			
ggg	atc	acc	aag	gat	gac	acc	gaa	gcc	acc	gat	gcg	atc	aac	gca	gcg	2201
Gly	Ile	Thr	Lys	Asp	Asp	Thr	Glu	Ala	Thr	Asp	Ala	Ile	Asn	Ala	Ala	
		485					490					495				
ttg	gag	cgt	atg	tac	gcc	gac	ggg	tcc	ttc	cag	cgt	ttc	ctc	acc	gag	2249
Leu	Glu	Arg	Met	Tyr	Ala	Asp	Gly	Ser	Phe	Gln	Arg	Phe	Leu	Thr	Glu	
	500					505					510					
aac	ctc	ggc	gag	gat	tcc	cag	ggt	gtc	cag	gag	ggc	acc	ccg	ggg	gac	2297
Asn	Leu	Gly	Glu	Asp	Ser	Gln	Val	Val	Gln	Glu	Gly	Thr	Pro	Gly	Asp	
515					520					525					530	
ctc	tcc	ttc	ctg	gac	gag	tgac	ctgacg	ggg	ccgaacg	ccc	gatgagc					2345
Leu	Ser	Phe	Leu	Asp	Glu											
			535													
atgcgtggcc	cccgcacccc	gggggtgccac	gcacatcac	tttcaccact	gatcccctac											2405
cggttccttac	cgaggagaaa	ttcccc	atg agt aca tta tgg gcg gat ctg ggt													2458
			Met Ser Thr Leu Trp Ala Asp Leu Gly													
			540													
ccg	tca	ctc	cta	ccc	gca	ttc	tgg	gtg	aca	atc	caa	ctc	acc	gtc	tat	2506
Pro	Ser	Leu	Leu	Pro	Ala	Phe	Trp	Val	Thr	Ile	Gln	Leu	Thr	Val	Tyr	
			550					555						560		
tcc	gcc	atc	gga	tcc	atg	atc	ctc	ggg	acc	atc	ctc	acc	gcc	atg	agg	2554
Ser	Ala	Ile	Gly	Ser	Met	Ile	Leu	Gly	Thr	Ile	Leu	Thr	Ala	Met	Arg	
			565					570						575		
gtg	tcc	ccg	gtg	aag	atc	ctg	cgc	agc	ata	tcc	acc	gcc	tac	atc	aac	2602
Val	Ser	Pro	Val	Lys	Ile	Leu	Arg	Ser	Ile	Ser	Thr	Ala	Tyr	Ile	Asn	
		580					585						590			
acg	gtc	cgt	aac	acc	cca	ctg	acc	ctg	gtg	atc	ctg	ttc	tgt	tcc	ttc	2650
Thr	Val	Arg	Asn	Thr	Pro	Leu	Thr	Leu	Val	Ile	Leu	Phe	Cys	Ser	Phe	
	595					600						605				
ggc	ctg	tat	cag	aat	ctc	ggg	ctc	acc	ctc	gcc	ggg	cgc	gac	agt	tcc	2698
Gly	Leu	Tyr	Gln	Asn	Leu	Gly	Leu	Thr	Leu	Ala	Gly	Arg	Asp	Ser	Ser	
610					615					620					625	
acc	ttt	ctg	gcc	gat	aac	aac	ttc	cgg	ctc	gcg	gtg	ctc	gga	ttc	atc	2746
Thr	Phe	Leu	Ala	Asp	Asn	Asn	Phe	Arg	Leu	Ala	Val	Leu	Gly	Phe	Ile	
			630					635						640		

ctg	tac	acc	tcc	gcc	ttc	gtt	gcg	gaa	tca	ctc	cgg	tca	ggc	atc	aac	2794				
Leu	Tyr	Thr	Ser	Ala	Phe	Val	Ala	Glu	Ser	Leu	Arg	Ser	Gly	Ile	Asn					
			645					650					655							
acc	gtg	cac	ttc	ggg	cag	gcg	gag	gcc	gcc	cgg	tcg	ctg	gga	ctc	ggg	2842				
Thr	Val	His	Phe	Gly	Gln	Ala	Glu	Ala	Ala	Arg	Ser	Leu	Gly	Leu	Gly					
		660					665					670								
ttc	agt	gac	atc	ttc	cgg	tcc	atc	atc	ttc	ccc	cag	gcg	gtg	cgt	gcc	2890				
Phe	Ser	Asp	Ile	Phe	Arg	Ser	Ile	Ile	Phe	Pro	Gln	Ala	Val	Arg	Ala					
	675					680					685									
gcc	atc	atc	ccg	ctg	ggc	aac	acc	ctc	atc	gcc	ctg	acc	aag	aac	acc	2938				
Ala	Ile	Ile	Pro	Leu	Gly	Asn	Thr	Leu	Ile	Ala	Leu	Thr	Lys	Asn	Thr					
690					695					700					705					
acg	atc	gcg	tcc	gtg	atc	ggc	gtc	ggg	gag	gcc	tcg	ctg	ctg	atg	aag	2986				
Thr	Ile	Ala	Ser	Val	Ile	Gly	Val	Gly	Glu	Ala	Ser	Leu	Leu	Met	Lys					
			710					715						720						
tcc	acg	att	gaa	aat	cat	gcc	aac	atg	ctc	ttc	gtc	gtg	ttc	gcc	atc	3034				
Ser	Thr	Ile	Glu	Asn	His	Ala	Asn	Met	Leu	Phe	Val	Val	Phe	Ala	Ile					
		725						730					735							
ttc	gcc	gtc	ggc	ttc	atg	atc	ctc	acc	ctc	ccc	atg	ggc	ctg	ggg	ctt	3082				
Phe	Ala	Val	Gly	Phe	Met	Ile	Leu	Thr	Leu	Pro	Met	Gly	Leu	Gly	Leu					
	740					745					750									
gga	aaa	ctc	gct	gag	aaa	atg	gcg	gtg	aag	aaa	taatgtcctc ctccgtacgc				3135					
Gly	Lys	Leu	Ala	Glu	Lys	Met	Ala	Val	Lys	Lys										
	755					760														
gcaacagtcc tctacgacgc ccccgggccc cggggacgca ggtccaacac catcatcacc																3195				
atcgccacca ccctggtggc agtggccgctc ctgttctgg gtg ggc agt gtt ctc																3249				
Val Gly Ser Val Leu																				
765																				
cag	gaa	aac	ggc	cag	ttg	gac	ggc	gac	aaa	tgg	acc	ccg	ttc	ctc	gat	3297				
Gln	Glu	Asn	Gly	Gln	Leu	Asp	Gly	Asp	Lys	Trp	Thr	Pro	Phe	Leu	Asp					
770					775					780					785					
ccc	cag	acc	tgg	acc	acc	tat	ctt	ctg	ccc	ggc	ctg	tgg	gga	acc	ctg	3345				
Pro	Gln	Thr	Trp	Thr	Thr	Tyr	Leu	Leu	Pro	Gly	Leu	Trp	Gly	Thr	Leu					
			790					795						800						
aag	gca	gcg	gtg	gcc	tcc	atc	ctt	ctc	gcg	ctg	atc	atg	ggc	acc	ctg	3393				
Lys	Ala	Ala	Val	Ala	Ser	Ile	Leu	Leu	Ala	Leu	Ile	Met	Gly	Thr	Leu					
			805					810					815							
ctc	ggg	ctc	gga	cgc	atc	tcc	gaa	atc	cgg	ctc	ctg	cgc	tgg	ttc	tgc	3441				
Leu	Gly	Leu	Gly	Arg	Ile	Ser	Glu	Ile	Arg	Leu	Leu	Arg	Trp	Phe	Cys					
		820					825					830								
ggg	atc	atc	atc	gag	acc	ttc	cgt	gcc	atc	ccg	gtg	ctg	atc	ctc	atg	3489				
Gly	Ile	Ile	Ile	Glu	Thr	Phe	Arg	Ala	Ile	Pro	Val	Leu	Ile	Leu	Met					
	835					840					845									
atc	ttc	gcc	tat	cag	ttg	ttc	gcc	cgt	tac	cag	ctc	gtt	cca	tca	cgc	3537				
Ile	Phe	Ala	Tyr	Gln	Leu	Phe	Ala	Arg	Tyr	Gln	Leu	Val	Pro	Ser	Arg					
850					855					860					865					
cag	ctg	gcc	ttc	gcc	gcg	gtg	gtc	ttc	ggg	ctc	acc	atg	tac	aac	ggc	3585				
Gln	Leu	Ala	Phe	Ala	Ala	Val	Val	Phe	Gly	Leu	Thr	Met	Tyr	Asn	Gly					
			870					875						880						
tcc	gtc	atc	gcc	gag	atc	ctt	aga	tcg	ggg	atc	gcc	tcc	ctg	ccg	aag	3633				
Ser	Val	Ile	Ala	Glu	Ile	Leu	Arg	Ser	Gly	Ile	Ala	Ser	Leu	Pro	Lys					

			885					890					895				
gga	cag	cgt	gag	gcg	gcg	atc	gcc	ctg	ggc	atg	tca	acc	cgc	cag	acc		3681
Gly	Gln	Arg	Glu	Ala	Ala	Ile	Ala	Leu	Gly	Met	Ser	Thr	Arg	Gln	Thr		
		900					905					910					
acc	tgg	tcg	atc	ctg	ctc	ccc	cag	gcg	gtg	gca	gcg	atg	ctg	ccc	gcc		3729
Thr	Trp	Ser	Ile	Leu	Leu	Pro	Gln	Ala	Val	Ala	Ala	Met	Leu	Pro	Ala		
	915					920					925						
ctg	atc	gcg	cag	atg	gtc	atc	gcg	ctg	aag	gac	tcc	gcc	ctc	ggc	tac		3777
Leu	Ile	Ala	Gln	Met	Val	Ile	Ala	Leu	Lys	Asp	Ser	Ala	Leu	Gly	Tyr		
930					935					940					945		
cag	atc	ggc	tat	atc	gag	gtg	gta	cgc	tcc	ggc	atc	cag	tcc	gca	tcc		3825
Gln	Ile	Gly	Tyr	Ile	Glu	Val	Val	Arg	Ser	Gly	Ile	Gln	Ser	Ala	Ser		
			950					955					960				
gtc	aac	cgg	aac	tac	ctg	gct	gcc	ctc	gcg	gtg	gtc	gcg	gtc	atc	atg		3873
Val	Asn	Arg	Asn	Tyr	Leu	Ala	Ala	Leu	Ala	Val	Val	Ala	Val	Ile	Met		
			965				970						975				
atc	ctg	atc	aac	ttc	gca	ctg	acc	gca	ctg	gca	gag	cgt	atc	cag	cgt		3921
Ile	Leu	Ile	Asn	Phe	Ala	Leu	Thr	Ala	Leu	Ala	Glu	Arg	Ile	Gln	Arg		
		980				985					990						
cag	ctg	cgt	gcc	gga	cgt	gcc	cgc	agg	aac	att	gtg	gca	aag	gtg	ccc		3969
Gln	Leu	Arg	Ala	Gly	Arg	Ala	Arg	Arg	Asn	Ile	Val	Ala	Lys	Val	Pro		
	995					1000					1005						
gag	gaa	ccc	gat	cag	ggc	ctg	gat	acc	aag	gac	aat	gtg	aac	gtg	gat		4017
Glu	Glu	Pro	Asp	Gln	Gly	Leu	Asp	Thr	Lys	Asp	Asn	Val	Asn	Val	Asp		
1010				1015				1020				1025					
tgg	cac	gat	ccc	gat	tac	aag	gaa	gtc	aaa	cac	ccg	gga	ccg	tca	ttc		4065
Trp	His	Asp	Pro	Asp	Tyr	Lys	Glu	Val	Lys	His	Pro	Gly	Pro	Ser	Phe		
			1030					1035				1040					
tgacaggtcc	ctggatcccc	gctgcggtca	ggaggcgggt	gcaacaatga	agtccgggctg												4125
cccagatgtc	tggggcagcc	ggactttgtg	gcagatcaat	gctgactgag	gtcctcgatg												4185
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<210> 17

<211> 242

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 17

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Leu	Thr	Asp	Ile	Asn	Leu	Glu	Val	Pro	Ala	Gly	Gln	Val	Val	Val	Val	
			20					25					30			
Leu	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Cys	Arg	Thr	Ile	Asn	
		35					40					45				
Arg	Leu	Glu	Thr	Ile	Glu	Glu	Gly	Thr	Ile	Glu	Ile	Asp	Gly	Lys	Leu	
	50					55					60					
Leu	Pro	Glu	Glu	Gly	Lys	Asp	Leu	Ala	Lys	Ile	Arg	Ala	Asp	Val	Gly	
65					70					75					80	
Met	Val	Phe	Gln	Ser	Phe	Asn	Leu	Phe	Pro	His	Leu	Thr	Ile	Lys	Asp	
				85					90					95		

Asn	Val	Thr	Leu	Gly	Pro	Met	Lys	Val	Arg	Lys	Met	Lys	Lys	Ser	Glu
			100					105					110		
Ala	Asn	Glu	Val	Ala	Met	Lys	Leu	Leu	Glu	Arg	Val	Gly	Ile	Ala	Asn
		115					120					125			
Gln	Ala	Glu	Lys	Tyr	Pro	Ala	Gln	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg
	130					135					140				
Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Met	Asn	Pro	Lys	Ile	Met	Leu	Phe
145					150					155					160
Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Glu	Met	Val	Asn	Glu	Val	Leu
			165						170					175	
Asp	Val	Met	Ala	Ser	Leu	Ala	Lys	Glu	Gly	Met	Thr	Met	Val	Cys	Val
			180					185					190		
Thr	His	Glu	Met	Gly	Phe	Ala	Arg	Arg	Ala	Ala	Asp	Arg	Val	Leu	Phe
		195					200					205			
Met	Ser	Asp	Gly	Ala	Ile	Val	Glu	Asp	Ser	Asp	Pro	Glu	Thr	Phe	Phe
	210					215					220				
Thr	Asn	Pro	Gln	Thr	Asp	Arg	Ala	Lys	Asp	Phe	Leu	Gly	Lys	Ile	Leu
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Ala	His														

<210> 18

<211> 294

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 18

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Ala	Val	Leu	Ala	Gly	Ile	Thr	Leu	Thr	Ala	Cys	Gly	Asp	Ser	Glu	Gly
			20					25					30		
Gly	Asp	Gly	Leu	Leu	Ala	Ala	Ile	Glu	Asn	Gly	Asn	Val	Thr	Ile	Gly
		35					40					45			
Thr	Lys	Tyr	Asp	Gln	Pro	Gly	Leu	Gly	Leu	Arg	Asn	Pro	Asp	Asn	Ser
	50					55					60				
Met	Ser	Gly	Leu	Asp	Val	Asp	Val	Ala	Gln	Tyr	Val	Val	Asn	Ser	Ile
65					70				75						80
Ala	Asp	Asp	Asn	Gly	Trp	Asp	His	Pro	Thr	Val	Glu	Trp	Arg	Glu	Thr
			85					90						95	
Pro	Ser	Ala	Gln	Arg	Glu	Thr	Leu	Ile	Gln	Asn	Gly	Glu	Val	Asp	Met
			100					105					110		
Ile	Ala	Ala	Thr	Tyr	Ser	Ile	Asn	Pro	Gly	Arg	Ser	Glu	Ser	Val	Asn
		115					120					125			
Phe	Gly	Gly	Pro	Tyr	Leu	Leu	Thr	His	Gln	Ala	Leu	Leu	Val	Arg	Glu
	130					135					140				
Asp	Asp	Asp	Arg	Ile	Gln	Thr	Leu	Glu	Asp	Leu	Asp	Asp	Gly	Leu	Ile
145					150					155					160
Leu	Cys	Ser	Val	Thr	Gly	Ser	Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val
			165						170					175	
Leu	Pro	Gly	Val	Gln	Leu	Gln	Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val
			180					185					190		
Glu	Ala	Leu	Ser	Gln	Gly	Asn	Val	Asp	Ala	Met	Thr	Thr	Asp	Ala	Thr

		195					200					205				
Ile	Leu	Phe	Gly	Tyr	Ala	Gln	Gln	Arg	Glu	Gly	Glu	Phe	Arg	Val	Val	
	210					215					220					
Glu	Met	Glu	Gln	Asp	Gly	Glu	Pro	Phe	Thr	Asn	Glu	Tyr	Tyr	Gly	Ile	
225					230					235					240	
Gly	Ile	Thr	Lys	Asp	Asp	Thr	Glu	Ala	Thr	Asp	Ala	Ile	Asn	Ala	Ala	
				245					250					255		
Leu	Glu	Arg	Met	Tyr	Ala	Asp	Gly	Ser	Phe	Gln	Arg	Phe	Leu	Thr	Glu	
			260					265					270			
Asn	Leu	Gly	Glu	Asp	Ser	Gln	Val	Val	Gln	Glu	Gly	Thr	Pro	Gly	Asp	
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Leu	Ser	Phe	Leu	Asp	Glu											
	290															

<210> 19

<211> 228

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 19

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			20					25					30			
Leu	Gly	Thr	Ile	Leu	Thr	Ala	Met	Arg	Val	Ser	Pro	Val	Lys	Ile	Leu	
		35				40						45				
Arg	Ser	Ile	Ser	Thr	Ala	Tyr	Ile	Asn	Thr	Val	Arg	Asn	Thr	Pro	Leu	
	50					55					60					
Thr	Leu	Val	Ile	Leu	Phe	Cys	Ser	Phe	Gly	Leu	Tyr	Gln	Asn	Leu	Gly	
65					70				75						80	
Leu	Thr	Leu	Ala	Gly	Arg	Asp	Ser	Ser	Thr	Phe	Leu	Ala	Asp	Asn	Asn	
				85				90						95		
Phe	Arg	Leu	Ala	Val	Leu	Gly	Phe	Ile	Leu	Tyr	Thr	Ser	Ala	Phe	Val	
			100					105					110			
Ala	Glu	Ser	Leu	Arg	Ser	Gly	Ile	Asn	Thr	Val	His	Phe	Gly	Gln	Ala	
		115					120					125				
Glu	Ala	Ala	Arg	Ser	Leu	Gly	Leu	Gly	Phe	Ser	Asp	Ile	Phe	Arg	Ser	
	130					135					140					
Ile	Ile	Phe	Pro	Gln	Ala	Val	Arg	Ala	Ala	Ile	Ile	Pro	Leu	Gly	Asn	
145					150					155					160	
Thr	Leu	Ile	Ala	Leu	Thr	Lys	Asn	Thr	Thr	Ile	Ala	Ser	Val	Ile	Gly	
				165					170					175		
Val	Gly	Glu	Ala	Ser	Leu	Leu	Met	Lys	Ser	Thr	Ile	Glu	Asn	His	Ala	
			180					185					190			
Asn	Met	Leu	Phe	Val	Val	Phe	Ala	Ile	Phe	Ala	Val	Gly	Phe	Met	Ile	
		195					200					205				
Leu	Thr	Leu	Pro	Met	Gly	Leu	Gly	Leu	Gly	Lys	Leu	Ala	Glu	Lys	Met	
	210					215						220				
Ala	Val	Lys	Lys													
225																

<210> 20
 <211> 277
 <212> PRT
 <213> Corynebacterium thermoaminogenes

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 Leu Trp Gly Thr Leu Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu
 35 40 45
 Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu
 50 55 60
 Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro
 65 70 75 80
 Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln
 85 90 95
 Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu
 100 105 110
 Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile
 115 120 125
 Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met
 130 135 140
 Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala
 145 150 155 160
 Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp
 165 170 175
 Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly
 180 185 190
 Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val
 195 200 205
 Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala
 210 215 220
 Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile
 225 230 235 240
 Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp
 245 250 255
 Asn Val Asn Val Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His
 260 265 270
 Pro Gly Pro Ser Phe
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<210> 21
 <211> 3598
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 <213> Corynebacterium thermoaminogenes

<220>
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<400> 21

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tccataatgt ggcctgtaac acccttgggc tcaaggcttc cacgccccac cgggaccctc 180
atcagcaggt gaaacagacc ctcttgcaat gctttgttaa aaagaaccgc cctttgtgcg 240
tatecttgtg tcaattgtgc gcgcactgcc accagctttc ctgaggattg aacacggtcg 300
ggaaatcctc cccggatacc ctgcacgccc cacctccac accgacaccg gcggggaggg 360
ccgggcacgt tttcagctgc gggatgatga agcggtcgcc ggtcccccg tgcataaac 420
gaaatgaaaa acattccaac aggaggtgtg gaa atg gcc gat caa gca aaa ctt 474
                                Met Ala Asp Gln Ala Lys Leu
                                1                               5

ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc 522
Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly
                                10                               15                               20

gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg 570
Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp
                                25                               30                               35

atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc 618
Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala
                                40                               45                               50                               55

cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc 666
Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val
                                60                               65                               70

cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca 714
Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr
                                75                               80                               85

tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac 762
Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr
                                90                               95                               100

cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag 810
Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln
                                105                               110                               115

cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc 858
Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala
                                120                               125                               130                               135

gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac 906
Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp
                                140                               145                               150

cac ccg ggt ggc ggt gac cag gtc ttc ttc cag ggt cac gcc tcc ccg 954
His Pro Gly Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro
                                155                               160                               165

ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat 1002
Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp
                                170                               175                               180

ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg 1050
Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro
                                185                               190                               195

tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc 1098
Ser Tyr Pro His Pro His Gly Met Pro Asp Phe Trp Glu Phe Pro Thr
                                200                               205                               210                               215

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gtg	tcc	atg	ggc	ctc	ggg	ccc	atg	gat	gcc	atc	tac	cag	gcg	cgc	ttc	1146
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			220						225					230		
aac	cgc	tac	ctg	cac	aac	cgt	ggc	atc	aag	gac	acc	tcg	gag	cag	cac	1194
Asn	Arg	Tyr	Leu	His	Asn	Arg	Gly	Ile	Lys	Asp	Thr	Ser	Glu	Gln	His	
			235					240					245			
gtc	tgg	gca	ttc	ctc	ggt	gac	ggc	gag	atg	gat	gag	ccg	gag	tcc	cgt	1242
Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu	Met	Asp	Glu	Pro	Glu	Ser	Arg	
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ggt	ctc	atc	cac	cag	gct	gcg	ctg	aac	aac	ctg	gac	aac	ctc	acc	ttc	1290
Gly	Leu	Ile	His	Gln	Ala	Ala	Leu	Asn	Asn	Leu	Asp	Asn	Leu	Thr	Phe	
		265				270					275					
gtg	atc	aac	tgc	aac	ctg	cag	cgt	ctt	gat	ggc	ccg	gtc	cgc	ggt	aac	1338
Val	Ile	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly	Asn	
					285					290					295	
acc	aag	atc	atc	cag	gaa	ctc	gag	tcc	ttc	ttc	cgt	ggt	gcc	ggc	tgg	1386
Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	Trp	
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tcc	gtc	atc	aag	gtc	atc	tgg	ggc	cgt	gag	tgg	gat	gaa	ctg	ctg	gag	1434
Ser	Val	Ile	Lys	Val	Ile	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	Glu	
			315					320					325			
aag	gac	cag	gac	ggt	gct	ctt	gtc	gag	gtc	atg	aac	aac	acc	tcc	gac	1482
Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Val	Met	Asn	Asn	Thr	Ser	Asp	
		330				335						340				
ggt	gac	tac	cag	acc	ttc	aag	gcc	aat	gac	ggt	gcc	tac	gtc	cgt	gag	1530
Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	Glu	
		345				350					355					
cac	ttc	ttc	ggc	cgt	gac	ccc	cgc	acc	ctc	aag	ctc	gtc	gag	gac	atg	1578
His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Leu	Lys	Leu	Val	Glu	Asp	Met	
					365					370					375	
acc	gac	gag	gag	atc	tgg	aag	ctg	ccc	cgt	ggt	ggc	cat	gac	tac	cgt	1626
Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	Arg	
				380					385					390		
aag	gtc	tac	gcc	gcc	tac	aag	cgt	gcg	ctg	gag	acc	aag	gac	cgc	ccg	1674
Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	Pro	
			395					400					405			
acc	gtc	att	ctc	gcc	cat	acc	atc	aag	ggc	tac	ggc	ctg	ggc	cac	aac	1722
Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	Asn	
		410					415					420				
ttc	gag	ggc	cgc	aac	gcg	acc	cac	cag	atg	aag	aag	ctg	acc	ctg	gat	1770
Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	Asp	
		425				430					435					
gac	ctg	aag	ctg	ttc	cgt	gac	aag	cag	ggt	ctg	ccc	atc	acc	gat	gag	1818
Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Leu	Pro	Ile	Thr	Asp	Glu	
					445				450						455	
gag	ctg	gag	aag	gat	ccc	tac	ctg	cct	ccg	tac	tac	cac	ccg	ggt	gag	1866
Glu	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	Glu	
				460				465						470		
gac	gca	ccg	gag	atc	aag	tac	atg	aag	gag	cgt	cgc	cag	gcg	ctc	ggt	1914
Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Gln	Ala	Leu	Gly	
			475					480					485			

ggt	ttc	ctg	ccg	gag	cgc	cgt	gag	aag	tac	gag	cca	ctg	cag	gtt	ccc	1962
Gly	Phe	Leu	Pro	Glu	Arg	Arg	Glu	Lys	Tyr	Glu	Pro	Leu	Gln	Val	Pro	
	490						495					500				
ccg	ctg	gac	aag	ctg	cgg	tcc	gtg	cgc	aag	ggt	tcc	ggc	aag	cag	cag	2010
Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	Gln	
	505					510					515					
gtg	gcc	acc	acc	atg	gcc	acg	gtg	cgt	acc	ttc	aag	gaa	ctc	atg	cgg	2058
Val	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	Arg	
520					525					530					535	
gac	aag	aac	ctg	gcc	gac	cgc	ttg	gtc	ccg	atc	atc	ccg	gat	gag	gcc	2106
Asp	Lys	Asn	Leu	Ala	Asp	Arg	Leu	Val	Pro	Ile	Ile	Pro	Asp	Glu	Ala	
				540					545					550		
cgc	acc	ttc	ggc	ctg	gac	tcc	tgg	ttc	ccg	acc	ctg	aaa	atc	tac	aac	2154
Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe	Pro	Thr	Leu	Lys	Ile	Tyr	Asn	
			555					560					565			
ccg	cac	ggt	cag	aac	tac	gtg	ccg	gtc	gac	cat	gac	ctc	atg	ctg	tcc	2202
Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val	Asp	His	Asp	Leu	Met	Leu	Ser	
		570					575					580				
tac	cgt	gag	gcc	aag	gac	ggc	cag	atc	ctg	cat	gag	ggc	atc	aac	gag	2250
Tyr	Arg	Glu	Ala	Lys	Asp	Gly	Gln	Ile	Leu	His	Glu	Gly	Ile	Asn	Glu	
	585					590					595					
gcc	ggt	tcc	gtg	gca	tcg	ttt	atc	gcc	gcc	gga	acc	tcc	tac	gcc	acc	2298
Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala	Ala	Gly	Thr	Ser	Tyr	Ala	Thr	
600					605					610					615	
cat	ggc	gag	gcc	atg	atc	ccg	ctg	tac	atc	ttc	tac	tcg	atg	ttc	ggc	2346
His	Gly	Glu	Ala	Met	Ile	Pro	Leu	Tyr	Ile	Phe	Tyr	Ser	Met	Phe	Gly	
				620					625					630		
ttc	cag	cgc	acc	ggt	gac	ggc	atc	tgg	gcc	gca	gcc	gac	cag	atg	acg	2394
Phe	Gln	Arg	Thr	Gly	Asp	Gly	Ile	Trp	Ala	Ala	Ala	Asp	Gln	Met	Thr	
			635					640					645			
cgt	ggt	ttc	ctc	ctg	ggc	gcc	acc	gcc	ggt	cgc	acc	acc	ctg	acc	ggt	2442
Arg	Gly	Phe	Leu	Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	
		650					655					660				
gag	ggc	ctc	cag	cac	atg	gat	ggc	cac	tcc	ccg	atc	ctg	gcc	tcc	acc	2490
Glu	Gly	Leu	Gln	His	Met	Asp	Gly	His	Ser	Pro	Ile	Leu	Ala	Ser	Thr	
	665					670					675					
aac	ccc	ggt	gtg	gag	acc	tat	gac	ccg	gcg	ttc	tcc	tac	gag	atc	gcg	2538
Asn	Pro	Gly	Val	Glu	Thr	Tyr	Asp	Pro	Ala	Phe	Ser	Tyr	Glu	Ile	Ala	
680					685					690					695	
cac	ctg	gtc	cac	cgc	ggc	atc	gac	cgc	atg	tac	gga	ccg	ggc	aag	ggt	2586
His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly	Lys	Gly	
				700					705					710		
gag	aat	gtc	atc	tac	tac	ctc	acc	atc	tac	aac	gag	cca	acc	ccg	cag	2634
Glu	Asn	Val	Ile	Tyr	Tyr	Leu	Thr	Ile	Tyr	Asn	Glu	Pro	Thr	Pro	Gln	
			715					720					725			
ccg	gct	gag	cct	gag	gat	ctg	gac	gtc	gag	ggc	ctg	cac	aag	ggc	atc	2682
Pro	Ala	Glu	Pro	Glu	Asp	Leu	Asp	Val	Glu	Gly	Leu	His	Lys	Gly	Ile	
		730					735					740				
tac	ctc	tac	gac	aag	gcc	gcc	gag	ggt	gag	ggc	cat	gag	gcc	tcg	atc	2730
Tyr	Leu	Tyr	Asp	Lys	Ala	Ala	Glu	Gly	Glu	Gly	His	Glu	Ala	Ser	Ile	
	745					750					755					

ctg gcc tcc ggc atc ggc atg cag tgg gca ctg cgc gcc cgt gac atc	2778
Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile	
760 765 770 775	
ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tcg	2826
Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser	
780 785 790	
tgg gtg gag ctg gcc cgc gac ggt gcc cgc cgt aac ctg gag gcg ctg	2874
Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu	
795 800 805	
cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag ctg	2922
Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu	
810 815 820	
aag aag ggt tcc ggc ccc tac gtc gcg gtg tcc gac ttc gcg acc gac	2970
Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp	
825 830 835	
ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc	3018
Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu	
840 845 850 855	
ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt	3066
Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg	
860 865 870	
tac ttc aac atc gac gcc gag tcc atc gtc gtg gcg gtc ctg cgc ggc	3114
Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly	
875 880 885	
ctg gtc cgc gag ggt gtc atc gat gcc tcc gtg gcg gcg cac gcg gct	3162
Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala	
890 895 900	
gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac	3210
Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp	
905 910 915	
gca ccg atc gag tagacctgct tgtcgacgaa aaacaccccc gccccctcac	3262
Ala Pro Ile Glu	
920	
atgatgaggg gggcgggggt gtgctcgttt acggcgggta caggggggta tcagcccagc	3322
atcgcccttat cggagagcgt cgcgcccttg atcttggcga attcctgcag cagatcccgc	3382
acggtgagct tctgcttcac ctctgcgctg gcctcataga cgateccgtcc ctcgtgcatc	3442
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gtcagtttgc cgtcctcgac gatcttctcg gtcagggtgg tgaccagttc ggctcgctgg	3562
gggtccaggg cggcgggtgtg ttcgtcgaga agcatg	3598

<210> 22

<211> 923

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 22

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1 5 10 15	
Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp	
20 25 30	
Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln	

		35				40				45					
Asp	Ser	Ser	Pro	Glu	Arg	Ala	Arg	Tyr	Leu	Met	Leu	Arg	Leu	Leu	Glu
	50					55					60				
Arg	Ala	Ser	Ala	Lys	Arg	Val	Pro	Leu	Pro	Pro	Met	Thr	Ser	Thr	Asp
65					70					75					80
Tyr	Val	Asn	Thr	Ile	Pro	Thr	Ser	Met	Glu	Pro	Asp	Phe	Pro	Gly	Asp
				85					90					95	
Glu	Glu	Met	Glu	Lys	Arg	Tyr	Arg	Arg	Trp	Met	Arg	Trp	Asn	Ala	Ala
			100					105					110		
Ile	Met	Val	His	Arg	Ala	Gln	Arg	Pro	Gly	Ile	Gly	Val	Gly	Gly	His
		115					120					125			
Ile	Ser	Thr	Tyr	Ala	Gly	Ala	Ala	Pro	Leu	Tyr	Glu	Val	Gly	Phe	Asn
	130					135					140				
His	Phe	Phe	Arg	Gly	Lys	Asp	His	Pro	Gly	Gly	Gly	Asp	Gln	Val	Phe
145					150					155					160
Phe	Gln	Gly	His	Ala	Ser	Pro	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Glu
				165					170					175	
Gly	Arg	Leu	Thr	Glu	Ser	Asp	Leu	Asp	Ser	Phe	Arg	Gln	Glu	Val	Ser
			180					185					190		
Tyr	Glu	Gly	Gly	Gly	Ile	Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Pro
		195					200					205			
Asp	Phe	Trp	Glu	Phe	Pro	Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp
	210					215					220				
Ala	Ile	Tyr	Gln	Ala	Arg	Phe	Asn	Arg	Tyr	Leu	His	Asn	Arg	Gly	Ile
225					230					235					240
Lys	Asp	Thr	Ser	Glu	Gln	His	Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu
				245					250					255	
Met	Asp	Glu	Pro	Glu	Ser	Arg	Gly	Leu	Ile	His	Gln	Ala	Ala	Leu	Asn
			260					265					270		
Asn	Leu	Asp	Asn	Leu	Thr	Phe	Val	Ile	Asn	Cys	Asn	Leu	Gln	Arg	Leu
		275					280					285			
Asp	Gly	Pro	Val	Arg	Gly	Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser
	290					295					300				
Phe	Phe	Arg	Gly	Ala	Gly	Trp	Ser	Val	Ile	Lys	Val	Ile	Trp	Gly	Arg
305					310					315					320
Glu	Trp	Asp	Glu	Leu	Leu	Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu
				325					330					335	
Val	Met	Asn	Asn	Thr	Ser	Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn
			340					345					350		
Asp	Gly	Ala	Tyr	Val	Arg	Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr
		355					360					365			
Leu	Lys	Leu	Val	Glu	Asp	Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro
	370					375					380				
Arg	Gly	Gly	His	Asp	Tyr	Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala
385					390					395					400
Leu	Glu	Thr	Lys	Asp	Arg	Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys
				405					410					415	
Gly	Tyr	Gly	Leu	Gly	His	Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln
			420					425					430		
Met	Lys	Lys	Leu	Thr	Leu	Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln
		435					440					445			

Gly	Leu	Pro	Ile	Thr	Asp	Glu	Glu	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro
	450					455				460					
Pro	Tyr	Tyr	His	Pro	Gly	Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys
465					470					475					480
Glu	Arg	Arg	Gln	Ala	Leu	Gly	Gly	Phe	Leu	Pro	Glu	Arg	Arg	Glu	Lys
				485					490					495	
Tyr	Glu	Pro	Leu	Gln	Val	Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg
			500					505					510		
Lys	Gly	Ser	Gly	Lys	Gln	Gln	Val	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg
		515					520					525			
Thr	Phe	Lys	Glu	Leu	Met	Arg	Asp	Lys	Asn	Leu	Ala	Asp	Arg	Leu	Val
	530					535					540				
Pro	Ile	Ile	Pro	Asp	Glu	Ala	Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe
545					550					555					560
Pro	Thr	Leu	Lys	Ile	Tyr	Asn	Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val
				565					570					575	
Asp	His	Asp	Leu	Met	Leu	Ser	Tyr	Arg	Glu	Ala	Lys	Asp	Gly	Gln	Ile
			580					585					590		
Leu	His	Glu	Gly	Ile	Asn	Glu	Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala
		595					600					605			
Ala	Gly	Thr	Ser	Tyr	Ala	Thr	His	Gly	Glu	Ala	Met	Ile	Pro	Leu	Tyr
	610					615					620				
Ile	Phe	Tyr	Ser	Met	Phe	Gly	Phe	Gln	Arg	Thr	Gly	Asp	Gly	Ile	Trp
625					630					635					640
Ala	Ala	Ala	Asp	Gln	Met	Thr	Arg	Gly	Phe	Leu	Leu	Gly	Ala	Thr	Ala
				645					650					655	
Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln	His	Met	Asp	Gly	His
			660					665					670		
Ser	Pro	Ile	Leu	Ala	Ser	Thr	Asn	Pro	Gly	Val	Glu	Thr	Tyr	Asp	Pro
		675					680					685			
Ala	Phe	Ser	Tyr	Glu	Ile	Ala	His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg
	690					695					700				
Met	Tyr	Gly	Pro	Gly	Lys	Gly	Glu	Asn	Val	Ile	Tyr	Tyr	Leu	Thr	Ile
705					710					715					720
Tyr	Asn	Glu	Pro	Thr	Pro	Gln	Pro	Ala	Glu	Pro	Glu	Asp	Leu	Asp	Val
				725					730					735	
Glu	Gly	Leu	His	Lys	Gly	Ile	Tyr	Leu	Tyr	Asp	Lys	Ala	Ala	Glu	Gly
			740					745					750		
Glu	Gly	His	Glu	Ala	Ser	Ile	Leu	Ala	Ser	Gly	Ile	Gly	Met	Gln	Trp
		755					760					765			
Ala	Leu	Arg	Ala	Arg	Asp	Ile	Leu	Ala	Glu	Asp	Tyr	Gly	Ile	Arg	Ala
	770					775					780				
Asn	Ile	Phe	Ser	Ala	Thr	Ser	Trp	Val	Glu	Leu	Ala	Arg	Asp	Gly	Ala
785					790					795					800
Arg	Arg	Asn	Leu	Glu	Ala	Leu	Arg	Asn	Pro	Gly	Ala	Asp	Val	Gly	Glu
				805					810					815	
Ala	Phe	Val	Thr	Thr	Gln	Leu	Lys	Lys	Gly	Ser	Gly	Pro	Tyr	Val	Ala
			820					825					830		
Val	Ser	Asp	Phe	Ala	Thr	Asp	Leu	Pro	Asn	Gln	Ile	Arg	Glu	Trp	Val
		835					840					845			
Pro	Gly	Asp	Tyr	Ile	Val	Leu	Gly	Ala	Asp	Gly	Phe	Gly	Phe	Ser	Asp

850	855	860
Thr Arg Pro Ala Ala Arg	Arg Tyr Phe Asn Ile	Asp Ala Glu Ser Ile
865	870	875
Val Val Ala Val Leu Arg	Gly Leu Val Arg Glu	Gly Val Ile Asp Ala
	885	890
Ser Val Ala Ala His Ala	Ala Glu Lys Tyr Lys	Leu Ser Asp Pro Thr
	900	905
Ala Pro Gln Val Asp Pro	Asp Ala Pro Ile Glu	
	915	920

<210> 23
 <211> 4013
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (319)..(3735)

<400> 23

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cggcaatggg	ggtctcgggc	gggggggcatt	ctttttcacgg	caaggtgggtg	aaattccgca	180
ggtcactccc	cggccggcgg	tagagaacgg	agcgaaaacg	gaaagcaata	cgtgggttttc	240
cggactggcc	gttacgatgt	tctgaagagt	gactgccatc	acccaacagg	ctggtcctcg	300
tcgaaaggaa	caaaaact	gtg gtt aca	aca aca ccc	tcc acg ctg	ccg gcg	351
		Val Val Thr	Thr Thr Pro	Ser Thr Leu	Pro Ala	
		1	5	10		
ttc aaa aag	atc ctg gtg	gcc aac cga	ggt gaa atc	gcg gtg cga	gca	399
Phe Lys Lys	Ile Leu Val	Ala Asn Arg	Gly Glu Ile	Ala Val Arg	Ala	
	15	20	25			
ttc cgc gcc	gcc tac gag	acc ggg gcc	gca acc gtg	gcc atc tac	ccc	447
Phe Arg Ala	Ala Tyr Glu	Thr Gly Ala	Ala Thr Val	Ala Ile Tyr	Pro	
	30	35	40			
cgg gag gac	cgt ggc tcc	ttc cac cgc	tcc ttc gcc	tcc gag gcg	gtg	495
Arg Glu Asp	Arg Gly Ser	Phe His Arg	Ser Phe Ala	Ser Glu Ala	Val	
	45	50	55			
agg atc gga	acc gag ggc	tca ccc gtc	aag gcg tac	ctc gat att	gat	543
Arg Ile Gly	Thr Glu Gly	Ser Pro Val	Lys Ala Tyr	Leu Asp Ile	Asp	
	60	65	70		75	
gag atc atc	aac gcc gcc	aag aag gtg	aaa gcg gac	gcg gtc tac	ccg	591
Glu Ile Ile	Asn Ala Ala	Lys Lys Val	Lys Ala Asp	Ala Val Tyr	Pro	
	80	85	90			
ggg tat ggt	ttc ctt tcg	gaa aat gcc	cag ctc gcg	cgt gaa tgc	gcg	639
Gly Tyr Gly	Phe Leu Ser	Glu Asn Ala	Gln Leu Ala	Arg Glu Cys	Ala	
	95	100	105			
gag aac ggc	att acc ttc	atc ggt ccc	acc ccg gag	gtg ctc gac	ctc	687
Glu Asn Gly	Ile Thr Phe	Ile Gly Pro	Thr Pro Glu	Val Leu Asp	Leu	
	110	115	120			
acg ggc gac	aag tcc aag	gct gtg tcc	gcc gcg aag	aag gcc ggg	ctg	735
Thr Gly Asp	Lys Ser Lys	Ala Val Ser	Ala Ala Lys	Lys Lys Ala	Gly Leu	

125	130	135	
ccg gtg ctg gcg gaa tcc acc ccc agc acc gac atc gat gag atc gtc 783			
Pro Val Leu Ala Glu Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val			
140	145	150	155
aag agt gcc gag ggg cag acc tac ccg atc ttc gtc aag gcc gtc gca 831			
Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala			
160	165	170	
ggg ggt ggc ggg cgt ggt atg cgg ttc gtc gag aag ccc gag gac ctg 879			
Gly Gly Gly Gly Arg Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu			
175	180	185	
cgt gag ctg gcc agg gag gcc tcc cgc gag gcg gag gcc gct ttc ggt 927			
Arg Glu Leu Ala Arg Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly			
190	195	200	
gac gga tcc gtc tac gtc gaa cgg gcc gtg atc aaa ccc cag cac atc 975			
Asp Gly Ser Val Tyr Val Glu Arg Ala Val Ile Lys Pro Gln His Ile			
205	210	215	
gag gtg cag atc ctc ggt gat cac acc ggc gat gtc atc cac ctg tat 1023			
Glu Val Gln Ile Leu Gly Asp His Thr Gly Asp Val Ile His Leu Tyr			
220	225	230	235
gaa cgc gac tgt tcc ctg cag cgc cgc cac cag aag gtc gtg gag atc 1071			
Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile			
240	245	250	
gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc 1119			
Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala			
255	260	265	
gat gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc 1167			
Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr			
270	275	280	
gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg 1215			
Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met			
285	290	295	
aac ccc cgc atc cag gtg gaa cac acc gtg acc gag gag gtc acc tcc 1263			
Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser			
300	305	310	315
gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg 1311			
Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu			
320	325	330	
aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc 1359			
Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala			
335	340	345	
ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc 1407			
Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro			
350	355	360	
gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gcg ggt gtg 1455			
Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val			
365	370	375	
cgt ctc gac ggc gca gcc cag ctc ggc ggc gag atc acc gca cat ttc 1503			
Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe			
380	385	390	395
gat tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc 1551			
Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr			

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gcc	gtg	tcc	cga	gcc	cag	cgc	gcc	ctg	gcg	gag	ttc	aac	gtc	tcc	ggc		1599
Ala	Val	Ser	Arg	Ala	Gln	Arg	Ala	Leu	Ala	Glu	Phe	Asn	Val	Ser	Gly		
			415					420					425				
gtg	gcc	acc	aac	atc	ggc	ttc	ctg	cgt	gcg	ctg	ctg	cgc	gag	gaa	gac		1647
Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp		
		430					435					440					
ttc	acc	aag	agg	cgc	atc	gac	acc	ggc	ttc	atc	ggc	tcc	cac	cag	cac		1695
Phe	Thr	Lys	Arg	Arg	Ile	Asp	Thr	Gly	Phe	Ile	Gly	Ser	His	Gln	His		
	445					450					455						
ctg	ctc	cag	gcc	cca	ccg	gcc	gac	gat	gag	cag	ggg	cgg	atc	ctg	gaa		1743
Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Glu		
460					465				470						475		
tac	ctg	gcg	gat	gtc	acc	gtg	aac	aaa	ccc	cac	ggt	gaa	cgc	ccc	gag		1791
Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys	Pro	His	Gly	Glu	Arg	Pro	Glu		
				480				485						490			
aca	gcc	cgt	ccg	ata	gag	aag	ctg	ccc	gag	gtg	gag	aac	atc	ccg	ctg		1839
Thr	Ala	Arg	Pro	Ile	Glu	Lys	Leu	Pro	Glu	Val	Glu	Asn	Ile	Pro	Leu		
			495					500					505				
cca	cgc	ggc	tcc	cgc	gac	cgc	ctg	aag	cag	ctc	ggc	ccg	gag	ggt	ttc		1887
Pro	Arg	Gly	Ser	Arg	Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Glu	Gly	Phe		
		510					515					520					
gcc	cgc	gat	ctg	cgc	gaa	cag	gat	gcc	ctg	gcc	gtc	acc	gac	acc	acc		1935
Ala	Arg	Asp	Leu	Arg	Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr		
	525					530					535						
ttc	cgc	gat	gcc	cac	cag	tcc	ctc	ctg	gcc	acc	cgc	gtg	cgc	tcc	ttc		1983
Phe	Arg	Asp	Ala	His	Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe		
540					545				550						555		
gcg	ctg	acc	ccg	gcg	gcg	cgc	gcc	gtc	gca	aag	ctc	acc	ccc	gag	ctg		2031
Ala	Leu	Thr	Pro	Ala	Ala	Arg	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu		
				560				565						570			
ctg	tcg	gtg	gag	gcc	tgg	ggc	ggt	gcc	acc	tac	gac	gtg	gcc	atg	cgc		2079
Leu	Ser	Val	Glu	Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg		
			575				580					585					
ttc	ctc	ttc	gag	gat	ccg	tgg	gca	cgc	ctg	gat	gag	ctg	cgt	gag	gcg		2127
Phe	Leu	Phe	Glu	Asp	Pro	Trp	Ala	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala		
		590					595					600					
atg	ccg	aat	gtg	aac	atc	cag	atg	ctg	ctg	cgt	ggt	cgc	aac	acc	gtc		2175
Met	Pro	Asn	Val	Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val		
	605					610					615						
ggg	tac	acc	ccg	tac	ccc	gat	tcg	gtg	tgc	cgc	gcg	ttt	gtg	cag	gag		2223
Gly	Tyr	Thr	Pro	Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Gln	Glu		
620					625				630						635		
gcc	gcc	aag	tcc	ggt	gtg	gac	atc	ttc	cgc	atc	ttc	gac	gcg	ctc	aac		2271
Ala	Ala	Lys	Ser	Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn		
				640				645						650			
gac	atc	tcc	cag	atg	cgc	ccg	gcc	atc	gac	gcc	gtc	ctg	gag	acc	ggc		2319
Asp	Ile	Ser	Gln	Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Gly		
			655				660					665					
acc	agt	gtt	gcc	gag	gtc	gcc	atg	gcg	tac	tcc	ggt	gac	ctg	tcc	aat		2367
Thr	Ser	Val	Ala	Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asn		

		670					675					680					
ccg	ggg	gag	aag	ctc	tac	acc	ctg	gac	tac	tac	ctg	aac	ctg	gcc	gag		2415
Pro	Gly	Glu	Lys	Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Asn	Leu	Ala	Glu		
	685						690					695					
cag	atc	gtc	gac	tcc	ggc	gca	cac	atc	ctg	gcc	atc	aag	gac	atg	gcc		2463
Gln	Ile	Val	Asp	Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	Lys	Asp	Met	Ala		
	700				705					710					715		
ggc	ctg	ctg	cgc	cgc	gcc	gcg	gcg	ccc	aaa	ctg	gtc	acc	gcc	ctg	cgc		2511
Gly	Leu	Leu	Arg	Arg	Ala	Ala	Ala	Pro	Lys	Leu	Val	Thr	Ala	Leu	Arg		
				720					725					730			
cgt	gaa	ttc	gac	ctg	ccc	gtg	cat	gtc	cac	acc	cac	gac	acc	gcc	ggc		2559
Arg	Glu	Phe	Asp	Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly		
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ggc	cag	ctg	gcc	acc	tac	ctg	gcc	gcc	gcc	aac	gcc	ggg	gcc	gat	gcc		2607
Gly	Gln	Leu	Ala	Thr	Tyr	Leu	Ala	Ala	Ala	Asn	Ala	Gly	Ala	Asp	Ala		
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gtc	gac	gcc	gcc	tcc	gca	ccc	ctg	tcc	ggc	acc	acc	tcc	cag	ccg	tcg		2655
Val	Asp	Ala	Ala	Ser	Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser		
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atg	tcc	gct	ctg	gtt	gcc	gcg	ttt	gcg	cac	acc	cga	cgc	gac	acc	ggc		2703
Met	Ser	Ala	Leu	Val	Ala	Ala	Phe	Ala	His	Thr	Arg	Arg	Asp	Thr	Gly		
	780				785					790					795		
ctc	aac	ctg	cag	gcc	gtc	tcc	gac	ctg	gaa	ccg	tac	tgg	gag	gcg	gtc		2751
Leu	Asn	Leu	Gln	Ala	Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val		
				800					805					810			
cgc	gga	ctg	tac	ctg	ccg	ttt	gaa	tcc	ggc	acc	ccg	ggc	ccg	acc	gga		2799
Arg	Gly	Leu	Tyr	Leu	Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly		
			815					820					825				
cgc	gtt	tac	cgc	cac	gag	atc	ccc	ggc	ggc	cag	ctg	tcc	aac	ctg	cgt		2847
Arg	Val	Tyr	Arg	His	Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg		
		830					835					840					
gcc	cag	gcc	gtt	gca	ctg	ggc	ctg	gcc	gac	cgc	ttc	gag	ctc	atc	gag		2895
Ala	Gln	Ala	Val	Ala	Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu		
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gac	tac	tac	gcg	gcc	gtc	aac	gag	atg	ctg	ggc	cgt	ccg	acc	aag	gtc		2943
Asp	Tyr	Tyr	Ala	Ala	Val	Asn	Glu	Met	Leu	Gly	Arg	Pro	Thr	Lys	Val		
	860				865					870					875		
acc	ccg	tcc	tcc	aag	gtt	gtc	ggc	gac	ctc	gca	ctg	cac	ctc	gtc	ggc		2991
Thr	Pro	Ser	Ser	Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly		
				880					885					890			
gcc	ggc	gtg	agc	ccg	gag	gat	ttc	gcc	gcc	gat	ccg	cag	aag	tac	gac		3039
Ala	Gly	Val	Ser	Pro	Glu	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp		
			895					900					905				
atc	ccc	gat	tcg	gtc	atc	gcc	ttc	ctc	cgc	ggc	gaa	ctg	ggc	acc	cct		3087
Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	Gly	Thr	Pro		
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Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu	Glu	Gly	Arg		
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Ser	Gln	Gly	Lys	Ala	Pro	Leu	Ala	Glu	Ile	Pro	Ala	Glu	Glu	Gln	Ala		

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His Leu Asp Ser Asp	Asp Ser Ala Glu Arg Arg	Gly Thr Leu Asn Arg					
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ctg ctg ttc ccg aag ccg acc gag gag	ttc ctt gag cac cgt	cgc cg	3279				
Leu Leu Phe Pro Lys Pro Thr Glu Glu	Phe Leu Glu His Arg Arg	Arg					
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Phe Gly Asn Thr Ser Ala Leu Asp	Arg Glu Phe Phe Tyr Gly	Leu					
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aag gag gga cgt gag gag ctg atc	cga ctg acc ggt gtg tcc acc ccg		3375				
Lys Glu Gly Arg Glu Glu Leu Ile	Arg Leu Thr Gly Val Ser Thr	Pro					
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atg gtg gtc cgc ctg gat gcg gtg	tcc gaa ccg gat gac aaa ggc	atg	3423				
Met Val Val Arg Leu Asp Ala Val	Ser Glu Pro Asp Asp Lys Gly	Met					
	1020		1025			1030	
cg	aac gtg gtg gtc aac gtc aac	ggc cag atc cgc ccg atc aag	gtg	3471			
Arg Asn Val Val Val Asn Val Asn	Gly Gln Ile Arg Pro Ile Lys	Val					
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cg	gac cgt tcc gtg gag tcc gtc acc	gcc acc gcg gag aag gcc	gat	3519			
Arg Asp Arg Ser Val Glu Ser Val	Thr Ala Thr Ala Glu Lys Ala	Asp					
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gcc acc aac aag ggc cat gtc gcc	gca cca ttc gcc ggt gtg gtc	acc	3567				
Ala Thr Asn Lys Gly His Val Ala	Ala Pro Phe Ala Gly Val Val	Thr					
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gtg acc gtc gcc gag ggt gat gag	atc aag gct ggc gac gcc gtg	gcc	3615				
Val Thr Val Ala Glu Gly Asp Glu	Ile Lys Ala Gly Asp Ala Val	Ala					
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Ile Ile Glu Ala Met Lys Met Glu	Ala Thr Ile Thr Ala Pro Val	Asp					
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ggt gtc atc gac cgc gtc gtg gtg	ccc gcc gcc acc aag gtc gag	ggc	3711				
Gly Val Ile Asp Arg Val Val Val	Pro Ala Ala Thr Lys Val Glu	Gly					
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ggc gac ctc atc gtg gtc gtg tcc	tagcgactga gagccacaac ccgtcccggg		3765				
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Glu	Thr	Gly	Ala	Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly
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Ser	Phe	His	Arg	Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu
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Gly	Ser	Pro	Val	Lys	Ala	Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Asn	Ala
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Ala	Lys	Lys	Val	Lys	Ala	Asp	Ala	Val	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu
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Ser	Glu	Asn	Ala	Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr
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Phe	Ile	Gly	Pro	Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser
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Lys	Ala	Val	Ser	Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu
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Ser	Thr	Pro	Ser	Thr	Asp	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly
145					150					155					160
Gln	Thr	Tyr	Pro	Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg
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Gly	Met	Arg	Phe	Val	Glu	Lys	Pro	Glu	Asp	Leu	Arg	Glu	Leu	Ala	Arg
			180					185					190		
Glu	Ala	Ser	Arg	Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ser	Val	Tyr
		195				200					205				
Val	Glu	Arg	Ala	Val	Ile	Lys	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu
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Gly	Asp	His	Thr	Gly	Asp	Val	Ile	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser
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Leu	Gln	Arg	Arg	His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His
				245					250					255	
Leu	Asp	Pro	Glu	Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe
			260					265					270		
Cys	Lys	Ser	Ile	Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val
		275				280						285			
Asp	Glu	Ala	Gly	Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln
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Val	Glu	His	Thr	Val	Thr	Glu	Glu	Val	Thr	Ser	Val	Asp	Leu	Val	Lys
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Ala	Gln	Met	His	Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu
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Thr	Gln	Asp	Lys	Ile	Thr	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile
			340					345					350		
Thr	Thr	Glu	Asp	Pro	Ser	Asn	Asn	Phe	Arg	Pro	Asp	Thr	Gly	Val	Ile
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Thr	Ala	Tyr	Arg	Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala
	370					375					380				
Ala	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val
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Lys	Met	Thr	Cys	Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ser	Arg	Ala
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Gln	Arg	Ala	Leu	Ala	Glu	Phe	Asn	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile

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Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Lys	Arg	Arg	
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Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Glu	Tyr	Leu	Ala	Asp	Val	
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Thr	Val	Asn	Lys	Pro	His	Gly	Glu	Arg	Pro	Glu	Thr	Ala	Arg	Pro	Ile	
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Glu	Lys	Leu	Pro	Glu	Val	Glu	Asn	Ile	Pro	Leu	Pro	Arg	Gly	Ser	Arg	
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Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Glu	Gly	Phe	Ala	Arg	Asp	Leu	Arg	
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Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr	Phe	Arg	Asp	Ala	His	
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Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe	Ala	Leu	Thr	Pro	Ala	
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Ala	Arg	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu	Leu	Ser	Val	Glu	Ala	
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Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	Phe	Leu	Phe	Glu	Asp	
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Pro	Trp	Ala	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	Met	Pro	Asn	Val	Asn	
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Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr	Pro	Tyr	
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Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Gln	Glu	Ala	Ala	Lys	Ser	Gly	
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Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asn	Pro	Gly	Glu	Lys	Leu	
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Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Asn	Leu	Ala	Glu	Gln	Ile	Val	Asp	Ser	
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Tyr	Leu	Ala	Ala	Ala	Asn	Ala	Gly	Ala	Asp	Ala	Val	Asp	Ala	Ala	Ser	
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Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	Ser	Pro		
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Pro	Leu	Ala	Glu	Ile	Pro	Ala	Glu	Glu	Gln	Ala	His	Leu	Asp	Ser	Asp		
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Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser		
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Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe	Tyr	Gly	Leu	Lys	Glu	Gly	Arg	Glu		
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His	Val	Ala	Ala	Pro	Phe	Ala	Gly	Val	Val	Thr	Val	Thr	Val	Ala	Glu		
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Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile	
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Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu	
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Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala	
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gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac	252
Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp	
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gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac	300
Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn	
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Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg	
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Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg	
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Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser	
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Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu	
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Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu	
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Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly	
225 230 235	
ggg gat atc ccc acc acg gcg atg gtc agg ccg gga tcc tgg atc ggc	828
Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly	
240 245 250 255	
ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac	876
Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr	

				260					265					270			
gcc	acc	cat	cgg	gcc	gcg	gag	acc	gtg	ctc	aag	tac	tac	gtc	aag	caa		924
Ala	Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Val	Lys	Gln		
				275					280					285			
ctg	cac	gcc	ctg	gaa	cac	gaa	ctc	agt	ctc	tcc	gac	cgg	atg	aac	gtc		972
Leu	His	Ala	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Val		
				290					295					300			
atc	agc	gat	gag	ctg	cgt	gtg	ctt	gcc	gat	gcc	ggc	cag	aat	gac	atg		1020
Ile	Ser	Asp	Glu	Leu	Arg	Val	Leu	Ala	Asp	Ala	Gly	Gln	Asn	Asp	Met		
				305					310					315			
ccc	agc	cgg	gtt	gat	gaa	ccc	tac	cgg	cgg	gcc	atc	cac	ggc	atg	cgt		1068
Pro	Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Ile	His	Gly	Met	Arg		
				320					325					330			335
ggc	cgg	atg	ctg	gcc	acc	acg	gcc	gcc	ctg	atc	ggc	gag	gag	gcg	gtc		1116
Gly	Arg	Met	Leu	Ala	Thr	Thr	Ala	Ala	Leu	Ile	Gly	Glu	Glu	Ala	Val		
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gag	ggc	acc	tgg	ttc	aag	acc	ttc	acg	ccc	tat	acc	gat	acc	cac	gag		1164
Glu	Gly	Thr	Trp	Phe	Lys	Thr	Phe	Thr	Pro	Tyr	Thr	Asp	Thr	His	Glu		
				355					360					365			
ttc	aaa	cgc	gac	ctc	gat	atc	gtg	gat	ggc	tcc	ctg	aga	atg	tcc	cgg		1212
Phe	Lys	Arg	Asp	Leu	Asp	Ile	Val	Asp	Gly	Ser	Leu	Arg	Met	Ser	Arg		
				370					375					380			
gat	gac	atc	atc	gcc	gat	gac	cgt	ctg	gcc	atg	ctg	cgc	tcg	gcc	ctg		1260
Asp	Asp	Ile	Ile	Ala	Asp	Asp	Arg	Leu	Ala	Met	Leu	Arg	Ser	Ala	Leu		
				385					390					395			
gac	agc	ttc	ggg	ttc	aac	ctc	tac	tcc	ctg	gat	ctg	cgc	cag	aat	tcc		1308
Asp	Ser	Phe	Gly	Phe	Asn	Leu	Tyr	Ser	Leu	Asp	Leu	Arg	Gln	Asn	Ser		
				400					405					410			415
gac	ggc	ttc	gag	gat	gtc	ctc	acc	gaa	ttg	ttc	gcc	acc	gcc	cag	acc		1356
Asp	Gly	Phe	Glu	Asp	Val	Leu	Thr	Glu	Leu	Phe	Ala	Thr	Ala	Gln	Thr		
				420					425					430			
gag	aag	aac	tac	cgc	ggg	ttg	acg	gag	gcg	gag	aag	ctg	gac	ctg	ctg		1404
Glu	Lys	Asn	Tyr	Arg	Gly	Leu	Thr	Glu	Ala	Glu	Lys	Leu	Asp	Leu	Leu		
				435					440					445			
atc	cgc	gaa	ctg	agc	aca	ccc	cgc	ccg	ctc	atc	ccg	cac	ggg	gac	ccg		1452
Ile	Arg	Glu	Leu	Ser	Thr	Pro	Arg	Pro	Leu	Ile	Pro	His	Gly	Asp	Pro		
				450					455					460			
gac	tac	tcc	gag	gcc	acc	aac	cgt	gaa	ctg	ggg	att	ttt	tcg	aag	gcc		1500
Asp	Tyr	Ser	Glu	Ala	Thr	Asn	Arg	Glu	Leu	Gly	Ile	Phe	Ser	Lys	Ala		
				465					470					475			
gcg	gag	gcc	gtg	cgt	aaa	ttc	ggc	cct	ctc	atg	gtg	ccg	cac	tgc	atc		1548
Ala	Glu	Ala	Val	Arg	Lys	Phe	Gly	Pro	Leu	Met	Val	Pro	His	Cys	Ile		
				480					485					490			495
atc	tcc	atg	gcc	tct	tcc	gtc	acg	gac	atc	ctc	gaa	ccg	atg	gtg	ctg		1596
Ile	Ser	Met	Ala	Ser	Ser	Val	Thr	Asp	Ile	Leu	Glu	Pro	Met	Val	Leu		
				500					505					510			
ctc	aag	gag	ttc	ggc	ctg	atc	cgg	gcc	aac	ggg	aag	aac	ccg	acg	ggc		1644
Leu	Lys	Glu	Phe	Gly	Leu	Ile	Arg	Ala	Asn	Gly	Lys	Asn	Pro	Thr	Gly		
				515					520					525			
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Ser	Val	Asp	Val	Ile	Pro	Leu	Phe	Glu	Thr	Ile	Asp	Asp	Leu	Gln	Arg		

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Tyr	Leu	Glu	Gln	Arg	Asp	Asn	Val	Gln	Glu	Val	Met	Leu	Gly	Tyr	Ser		
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gac	tcc	aac	aag	gac	ggc	ggg	tac	ttc	gcc	gcc	aac	tgg	gcg	ctt	tac	1836	
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580			585			590											
gac	gcg	gag	tta	cgc	ctg	gtc	gaa	cta	tgc	cgg	ggc	cgt	aat	gtc	aag	1884	
Asp	Ala	Glu	Leu	Arg	Leu	Val	Glu	Leu	Cys	Arg	Gly	Arg	Asn	Val	Lys		
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Leu	Arg	Leu	Phe	His	Gly	Arg	Gly	Gly	Thr	Val	Gly	Arg	Gly	Gly	Gly		
610			615			620											
ccc	tcc	tat	gat	gcg	atc	ctg	gcc	cag	ccc	aag	ggc	gcg	gtc	cgg	ggc	1980	
Pro	Ser	Tyr	Asp	Ala	Ile	Leu	Ala	Gln	Pro	Lys	Gly	Ala	Val	Arg	Gly		
625			630			635											
gcg	gtg	cgg	gtg	act	gaa	cag	ggc	gag	atc	atc	tcc	gcg	aag	tac	ggc	2028	
Ala	Val	Arg	Val	Thr	Glu	Gln	Gly	Glu	Ile	Ile	Ser	Ala	Lys	Tyr	Gly		
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aac	ccg	gat	acg	gca	cgc	cgc	aac	ctt	gag	gcc	ctg	gtg	tcc	gcg	acg	2076	
Asn	Pro	Asp	Thr	Ala	Arg	Arg	Asn	Leu	Glu	Ala	Leu	Val	Ser	Ala	Thr		
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Leu	Glu	Ala	Ser	Leu	Leu	Asp	Asp	Val	Glu	Leu	Pro	Asn	Arg	Glu	Arg		
675			680			685											
gcg	cac	cag	atc	atg	ggg	gag	atc	tcg	gag	ttg	agc	ttc	cgc	agg	tac	2172	
Ala	His	Gln	Ile	Met	Gly	Glu	Ile	Ser	Glu	Leu	Ser	Phe	Arg	Arg	Tyr		
690			695			700											
tca	tca	ctg	gtc	cat	gag	gat	ccc	gga	ttc	atc	cag	tac	ttc	acc	cag	2220	
Ser	Ser	Leu	Val	His	Glu	Asp	Pro	Gly	Phe	Ile	Gln	Tyr	Phe	Thr	Gln		
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Ser	Thr	Pro	Leu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	Ile	Gly	Ser	Arg	Pro		
720			725			730									735		
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Ser	Ser	Arg	Lys	Gln	Thr	Asn	Thr	Val	Glu	Asp	Leu	Arg	Ala	Ile	Pro		
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tgg	gtg	ctc	agc	tgg	tcc	cag	tcc	cgt	gtc	atg	ctg	ccg	ggc	tgg	ttc	2364	
Trp	Val	Leu	Ser	Trp	Ser	Gln	Ser	Arg	Val	Met	Leu	Pro	Gly	Trp	Phe		
755			760			765											
ggc	gtg	ggc	acc	gca	ctg	cgt	gag	tgg	atc	ggc	gag	ggg	gag	ggg	gct	2412	
Gly	Val	Gly	Thr	Ala	Leu	Arg	Glu	Trp	Ile	Gly	Glu	Gly	Glu	Gly	Ala		
770			775			780											
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Ala	Glu	Arg	Ile	Ala	Glu	Leu	Gln	Glu	Leu	Asn	Arg	Cys	Trp	Pro	Phe		
785			790			795											
ttc	acc	tcg	gtg	ctg	gac	aac	atg	gcc	cag	gtg	atg	agc	aag	gcg	gaa	2508	
Phe	Thr	Ser	Val	Leu	Asp	Asn	Met	Ala	Gln	Val	Met	Ser	Lys	Ala	Glu		

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 Leu Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val
 810
 gcg gac cgg atc tat gag acc atc ttc ggg gag tat ttc ctg acc aag 2604
 Ala Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys
 820
 gag atg ttc tgc acc atc acc ggt tcc cag gac ctg ctc gat gac aac 2652
 Glu Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn
 835
 ccg gcg ctg gcg cga tcg gtg cgc agt cgg ttc ccg tac ctg ctg ccg 2700
 Pro Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro
 840
 ctc aat gtc atc cag gtg gag atg atg cgc cgg tac cgg tcc ggt gat 2748
 Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp
 845
 gag ggc acg gct gtc cca cgt aat atc cgc ctg acc atg aat gga ttg 2796
 Glu Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu
 850
 tcc acg gcc ctg cgc aac tcg ggt tagggcgcca gacgccccgg gaaccgcac 2850
 Ser Thr Ala Leu Arg Asn Ser Gly
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 35 40 45
 Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala
 50 55 60
 Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu
 65 70 75 80
 Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser
 85 90 95
 Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu
 100 105 110

Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn
 115 120 125
 Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg
 130 135 140
 Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu
 145 150 155 160
 Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys
 165 170 175
 Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp
 180 185 190
 Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val
 195 200 205
 Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro
 210 215 220
 Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly
 225 230 235 240
 Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly
 245 250 255
 Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala
 260 265 270
 Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu
 275 280 285
 His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile
 290 295 300
 Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro
 305 310 315 320
 Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg Gly
 325 330 335
 Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu
 340 345 350
 Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe
 355 360 365
 Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp
 370 375 380
 Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp
 385 390 395 400
 Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp
 405 410 415
 Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
 420 425 430
 Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile
 435 440 445
 Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp
 450 455 460
 Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala
 465 470 475 480
 Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
 485 490 495
 Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu
 500 505 510
 Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser

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Ser	Asn	Lys	Asp	Gly	Gly	Tyr	Phe	Ala	Ala	Asn	Trp	Ala	Leu	Tyr	Asp
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Ala	Glu	Leu	Arg	Leu	Val	Glu	Leu	Cys	Arg	Gly	Arg	Asn	Val	Lys	Leu
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Arg	Leu	Phe	His	Gly	Arg	Gly	Gly	Thr	Val	Gly	Arg	Gly	Gly	Gly	Pro
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Ser	Tyr	Asp	Ala	Ile	Leu	Ala	Gln	Pro	Lys	Gly	Ala	Val	Arg	Gly	Ala
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Val	Arg	Val	Thr	Glu	Gln	Gly	Glu	Ile	Ile	Ser	Ala	Lys	Tyr	Gly	Asn
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Pro	Asp	Thr	Ala	Arg	Arg	Asn	Leu	Glu	Ala	Leu	Val	Ser	Ala	Thr	Leu
			660					665					670		
Glu	Ala	Ser	Leu	Leu	Asp	Asp	Val	Glu	Leu	Pro	Asn	Arg	Glu	Arg	Ala
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His	Gln	Ile	Met	Gly	Glu	Ile	Ser	Glu	Leu	Ser	Phe	Arg	Arg	Tyr	Ser
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Ser	Leu	Val	His	Glu	Asp	Pro	Gly	Phe	Ile	Gln	Tyr	Phe	Thr	Gln	Ser
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Thr	Pro	Leu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	Ile	Gly	Ser	Arg	Pro	Ser
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Ser	Arg	Lys	Gln	Thr	Asn	Thr	Val	Glu	Asp	Leu	Arg	Ala	Ile	Pro	Trp
			740					745					750		
Val	Leu	Ser	Trp	Ser	Gln	Ser	Arg	Val	Met	Leu	Pro	Gly	Trp	Phe	Gly
		755					760					765			
Val	Gly	Thr	Ala	Leu	Arg	Glu	Trp	Ile	Gly	Glu	Gly	Glu	Gly	Ala	Ala
	770					775					780				
Glu	Arg	Ile	Ala	Glu	Leu	Gln	Glu	Leu	Asn	Arg	Cys	Trp	Pro	Phe	Phe
785					790					795					800
Thr	Ser	Val	Leu	Asp	Asn	Met	Ala	Gln	Val	Met	Ser	Lys	Ala	Glu	Leu
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Arg	Leu	Ala	Arg	Leu	Tyr	Ala	Asp	Leu	Ile	Pro	Asp	Arg	Glu	Val	Ala
			820					825					830		
Asp	Arg	Ile	Tyr	Glu	Thr	Ile	Phe	Gly	Glu	Tyr	Phe	Leu	Thr	Lys	Glu
		835					840					845			
Met	Phe	Cys	Thr	Ile	Thr	Gly	Ser	Gln	Asp	Leu	Leu	Asp	Asp	Asn	Pro
	850					855				860					
Ala	Leu	Ala	Arg	Ser	Val	Arg	Ser	Arg	Phe	Pro	Tyr	Leu	Leu	Pro	Leu
865					870					875					880
Asn	Val	Ile	Gln	Val	Glu	Met	Met	Arg	Arg	Tyr	Arg	Ser	Gly	Asp	Glu
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Gly	Thr	Ala	Val	Pro	Arg	Asn	Ile	Arg	Leu	Thr	Met	Asn	Gly	Leu	Ser
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 gaagaatacg ttaaataatca acaagaggat tacgaatctg atatttttaga aaaacgtgaa 360
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 tatagaaatt caagggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712
 Met Ala Ser Asn Phe Lys Glu Thr Ala
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 aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760
 Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu 25
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 aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808
 Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr 40
 30 35
 tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856
 Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe 55
 45 50
 gta att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904
 Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys 70
 60 65
 ggt aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952
 Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln 80
 75 85
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 Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys 100
 90 95
 gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gta 1048
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 Pro Val Asp Leu Val Ile Asp His Ser Val Gln Val Asp Ser Tyr Ala 135
 125 130
 aat cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac 1144
 Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn

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Tyr	Glu	Arg	Tyr	Gln	Phe	Leu	Asn	Trp	Ala	Thr	Lys	Ala	Phe	Asp	Asn	
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Tyr	Asn	Ala	Val	Pro	Pro	Ala	Thr	Gly	Ile	Val	His	Gln	Val	Asn	Leu	
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Glu	Tyr	Leu	Ala	Asn	Val	Val	His	Val	Arg	Asp	Val	Asp	Gly	Glu	Gln	
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Thr	Ala	Phe	Pro	Asp	Thr	Leu	Val	Gly	Thr	Asp	Ser	His	Thr	Thr	Met	
			205					210					215			
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Ile	Asn	Gly	Ile	Gly	Val	Leu	Gly	Trp	Gly	Val	Gly	Gly	Ile	Glu	Ala	
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Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val	
475 480 485	
gag aag tac ctg gca gac cac gac acc gag ggc ctg gac atc cag atc	1842
Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile	
490 495 500 505	
ctc tcc ccc gtc gag gcc acc cag cac gcc atc gac cgc atc cgc cgc	1890
Leu Ser Pro Val Glu Ala Thr Gln His Ala Ile Asp Arg Ile Arg Arg	
510 515 520	
ggc gag gac acc atc tcc gtc acc ggt aac gtc ctg cgt gac tac aac	1938
Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn	
525 530 535	
acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag atg ctc	1986
Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu	
540 545 550	
tcc gtc gtg cca ctg atg gcc ggc ggt gga ctc ttc gag acc ggt gcc	2034
Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala	
555 560 565	
ggt ggc tcc gcc ccg aag cac gtc cag cag gtc atc gag gaa aac cac	2082
Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Ile Glu Glu Asn His	
570 575 580 585	
ctg cgc tgg gat tcc ctc ggt gag ttc ctg gcc ctg gcc gag tcc ttc	2130
Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe	
590 595 600	
cgc cac gag ctc aac acc cgc aac aac acc aag gcc ggt gtc ctc gcc	2178
Arg His Glu Leu Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala	
605 610 615	
gat gcc ctg gac cgt gcg acc gag aag ctc ctc aac gag gag aag tcc	2226
Asp Ala Leu Asp Arg Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser	
620 625 630	

ccg	tcc	cgc	aag	gtc	ggc	gag	atc	gac	aac	cgt	ggt	tcc	cac	ttc	tgg	2274
Pro	Ser	Arg	Lys	Val	Gly	Glu	Ile	Asp	Asn	Arg	Gly	Ser	His	Phe	Trp	
635						640					645					
ctg	gcc	acc	tac	tgg	gcc	gat	gaa	ctg	gcc	aac	cag	acc	gag	gac	gcc	2322
Leu	Ala	Thr	Tyr	Trp	Ala	Asp	Glu	Leu	Ala	Asn	Gln	Thr	Glu	Asp	Ala	
650					655					660					665	
gag	ctg	gct	gag	acc	ttc	gcc	cct	gtc	gcc	gag	gcc	ctg	aac	aac	cag	2370
Glu	Leu	Ala	Glu	Thr	Phe	Ala	Pro	Val	Ala	Glu	Ala	Leu	Asn	Asn	Gln	
				670					675					680		
gct	gcc	gac	atc	gac	gca	gca	ctc	atc	ggt	gag	cag	ggc	aag	cct	gtc	2418
Ala	Ala	Asp	Ile	Asp	Ala	Ala	Leu	Ile	Gly	Glu	Gln	Gly	Lys	Pro	Val	
			685					690					695			
gac	ctg	ggt	ggc	tac	tac	gca	ccc	tcc	gat	gag	aag	acc	tcc	gcg	atc	2466
Asp	Leu	Gly	Gly	Tyr	Tyr	Ala	Pro	Ser	Asp	Glu	Lys	Thr	Ser	Ala	Ile	
		700					705					710				
atg	cgc	ccg	gtg	gcc	gca	ttc	aac	gag	atc	atc	gac	tcc	ctg	aag	aag	2514
Met	Arg	Pro	Val	Ala	Ala	Phe	Asn	Glu	Ile	Ile	Asp	Ser	Leu	Lys	Lys	
		715				720					725					
taacccccttc	tccggagccg	acagccgacg	gccacgctcc	cccgcccacg	ggggatcgtg	2574										
gccgctcgcc	gtttctggca	ctggagtga	cacttcggtg	ataatggtga	gatgaacagc	2634										
ccccgtgtcc	ccgccatcct	gtccgcccgtt	tccgcccgtg	gtctgatcgc	tgcgctgggc	2694										
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agccagaatg	acaactccag	cgtgatcagg	ttctgggatg	acctggaggc	cgatgtccgt	2814										
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ttcatcgccg	aggacccggt	agccccctcc	gcagccgatc	tccagagacg	gctggatgca	2934										
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<210> 30

<211> 729

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 30

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			20					25					30			
Ile	Glu	Val	Glu	Thr	Arg	Asp	Ile	Ser	Leu	Ala	Gly	Arg	Ile	Leu	Ala	
		35				40					45					
Gln	Phe	Ala	Asp	Gln	Leu	Pro	Glu	Glu	Gln	Lys	Val	Ser	Asp	Ala	Leu	
	50				55				60							
Ala	Glu	Leu	Gly	Glu	Leu	Ala	Lys	Thr	Pro	Glu	Ala	Asn	Ile	Ile	Lys	
	65			70					75					80		
Leu	Pro	Asn	Ile	Ser	Ala	Ser	Val	Pro	Gln	Leu	Lys	Ala	Ala	Val	Lys	
			85					90						95		
Glu	Leu	Gln	Glu	Gln	Gly	Tyr	Asp	Leu	Pro	Glu	Tyr	Glu	Asp	Ala	Lys	
		100					105						110			
Asp	Arg	Tyr	Ala	Ala	Val	Ile	Gly	Ser	Asn	Val	Asn	Pro	Val	Leu	Arg	
		115				120						125				
Glu	Gly	Asn	Ser	Asp	Arg	Arg	Ala	Pro	Val	Ala	Val	Lys	Asn	Phe	Val	

130 135 140
 Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala Asp Ser Lys Thr
 145 150 155 160
 Asn Val Ala Thr Met Gly Ala Asp Asp Phe Arg Ser Asn Glu Lys Ser
 165 170 175
 Val Ile Met Asp Glu Ala Asp Thr Val Val Ile Lys His Val Ala Ala
 180 185 190
 Asp Gly Thr Glu Thr Val Leu Lys Asp Ser Leu Pro Leu Leu Lys Gly
 195 200 205
 Glu Val Ile Asp Gly Thr Phe Ile Ser Ala Lys Ala Leu Asp Ala Phe
 210 215 220
 Leu Leu Asp Gln Val Lys Arg Ala Lys Glu Glu Gly Ile Leu Phe Ser
 225 230 235 240
 Ala His Met Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe
 245 250 255
 Gly His Ile Val Arg Ala Tyr Phe Ala Asp Val Tyr Ala Gln Tyr Gly
 260 265 270
 Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala
 275 280 285
 Ile Tyr Ala Gly Leu Asp Lys Leu Asp Asn Gly Ala Glu Ile Lys Ala
 290 295 300
 Ala Phe Asp Lys Gly Leu Glu Glu Gly Pro Asp Leu Ala Met Val Asn
 305 310 315 320
 Ser Ala Lys Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Ile
 325 330 335
 Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly Lys Met Trp Asn
 340 345 350
 Lys Asp Asp Gln Thr Gln Asp Ala Leu Ala Val Ile Pro Asp Ser Ser
 355 360 365
 Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly
 370 375 380
 Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met
 385 390 395 400
 Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile
 405 410 415
 Glu Ala Asp Gly Lys Val Gln Val Val Ala Ser Asn Gly Asp Val Leu
 420 425 430
 Ile Glu His Asp Val Glu Lys Gly Asp Ile Trp Arg Ala Cys Gln Thr
 435 440 445
 Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Asn Arg Ala
 450 455 460
 Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Ala Arg Ala
 465 470 475 480
 His Asp Arg Asn Leu Thr Thr Leu Val Glu Lys Tyr Leu Ala Asp His
 485 490 495
 Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro Val Glu Ala Thr
 500 505 510
 Gln His Ala Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val
 515 520 525
 Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu Phe Pro Ile Leu
 530 535 540

Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val Pro Leu Met Ala
 545 550 555 560
 Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His
 565 570 575
 Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly
 580 585 590
 Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg
 595 600 605
 Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr
 610 615 620
 Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu
 625 630 635 640
 Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp
 645 650 655
 Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala
 660 665 670
 Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala
 675 680 685
 Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala
 690 695 700
 Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe
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 Asn Glu Ile Ile Asp Ser Leu Lys Lys
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 <211> 2322
 <212> DNA
 <213> *Corynebacterium thermoaminogenes*

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 <221> CDS
 <222> (806)..(2212)

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 cctagcctct gccgatgcta aaagtcagct gacccttgg ggcgcttcat ttgaaactgc 180
 gaccaagctc atgaatgcgc gaaagcattt ccattataag ggtaagctgt aagaatagtg 240
 ggagaaaatg ttcagtcgtg ttctaactca cttgagaaat tccatttttc tgggcttctc 300
 tcaaatagat taagtggccc gtatgctgga tttctagaat atttagaagc gcgccaaactc 360
 atgattatgt attgtataag cctcaaagac cgaatagatt actaacattt aagtggacca 420
 gagcgttaga agctttgtag agtgctcatt ccttgctgac ggcaagggtt tcctaccatg 480
 agatagatcg gcagatagtt ggtttgtaaa aattttttaag gacggtccgc aatgtcaatt 540
 cttgaacaga tcatcttctt catcaacacc atcttgggtt atggtctgca cgctggttct 600
 tccgcttcca gcaacctttc tcacacgata ggctgttct aggcctaatt ggtaataagg 660
 ctgtgtaaca gtcgcccgcg tgattgtgtc tttttaggcg cccgcgcggg cgattttcgg 720
 ttttcatctt ttttaaattg agtttggaag atcaagtgcc cccggatgca cgacaatgct 780
 atgccgaaca cgtattgttg aaatc gtg act gaa cat tat gac gta gta gta 832
 Val Thr Glu His Tyr Asp Val Val Val

ctc	gga	gct	ggc	ccc	ggt	ggc	tat	gtc	tcc	gcc	atc	cgc	gcc	gcg	cag	880
Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	Arg	Ala	Ala	Gln	
10					15					20					25	
ctc	ggt	aag	aaa	gtt	gcg	gtt	atc	gag	aag	cag	tac	tgg	gga	ggt	gtc	928
Leu	Gly	Lys	Lys	Val	Ala	Val	Ile	Glu	Lys	Gln	Tyr	Trp	Gly	Gly	Val	
				30					35					40		
tgc	ctg	aat	gtg	ggt	tgt	atc	cca	tct	aag	gcg	ttg	atc	aag	aac	gct	976
Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Ile	Lys	Asn	Ala	
			45					50					55			
gag	atc	gcc	cac	atc	ttc	aac	cat	gag	aag	aag	acc	ttc	ggc	atc	aac	1024
Glu	Ile	Ala	His	Ile	Phe	Asn	His	Glu	Lys	Lys	Thr	Phe	Gly	Ile	Asn	
		60				65					70					
ggc	gag	gtc	acc	ttc	aac	tac	gag	gat	gcc	cac	aag	cgt	tcc	cgt	ggt	1072
Gly	Glu	Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	
	75					80					85					
gtc	tcc	gac	aag	atc	gtc	ggc	ggt	gtt	cac	tac	ttg	atg	aag	aag	aac	1120
Val	Ser	Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	
	90				95					100					105	
aag	atc	acc	gag	atc	gac	ggt	ttc	ggc	acc	ttc	aag	gat	gcc	aag	acc	1168
Lys	Ile	Thr	Glu	Ile	Asp	Gly	Phe	Gly	Thr	Phe	Lys	Asp	Ala	Lys	Thr	
				110				115						120		
atc	gag	gtg	acc	gat	ggt	aag	gat	gcc	ggc	aag	acc	gtc	acc	ttc	gat	1216
Ile	Glu	Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Val	Thr	Phe	Asp	
			125					130					135			
gac	tgc	atc	atc	gcc	acc	ggt	tcc	gtg	gtc	aac	tcc	ctc	cgt	ggt	gtt	1264
Asp	Cys	Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Ser	Leu	Arg	Gly	Val	
		140					145					150				
gag	ttc	tcc	gag	aac	gtg	gtc	tcc	tac	gag	gag	cag	atc	ctc	aac	ccg	1312
Glu	Phe	Ser	Glu	Asn	Val	Val	Ser	Tyr	Glu	Glu	Gln	Ile	Leu	Asn	Pro	
	155					160					165					
gtg	gcg	cct	aag	aag	atg	gtc	atc	gtc	ggt	ggc	ggc	gcc	atc	ggt	atg	1360
Val	Ala	Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Gly	Gly	Ala	Ile	Gly	Met	
	170				175					180					185	
gaa	ttc	gcc	tac	gtt	ctg	ggc	aac	tac	ggt	gtg	gac	gta	acc	ctc	atc	1408
Glu	Phe	Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Leu	Ile	
				190					195					200		
gag	ttc	atg	gac	cgc	gtt	ctg	ccg	aac	gag	gat	cca	gag	gtg	tcc	aag	1456
Glu	Phe	Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Pro	Glu	Val	Ser	Lys	
			205					210					215			
gtt	atc	gcc	aag	gcc	tac	aag	aag	atg	ggc	atc	aag	ctc	ctc	ccg	ggc	1504
Val	Ile	Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Ile	Lys	Leu	Leu	Pro	Gly	
		220				225						230				
cac	gca	acc	acc	gcg	gtg	cgc	gac	aat	ggc	gat	tcc	gtt	gag	gtc	gat	1552
His	Ala	Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Ser	Val	Glu	Val	Asp	
	235					240					245					
tac	cag	aag	aag	ggc	tcg	gac	aag	acc	gag	acc	atc	acc	gtc	gac	cgt	1600
Tyr	Gln	Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Ile	Thr	Val	Asp	Arg	
	250				255					260					265	
gtt	ctt	atc	tcc	gtc	ggc	ttc	cgc	cca	cgc	gtc	gag	ggc	ttc	ggc	ctg	1648
Val	Leu	Ile	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	
				270					275					280		

gag aac acc ggc gtc aag ctc acc gaa cgc ggt gcc atc gac att gat	1696
Glu Asn Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Asp Ile Asp	
285 290 295	
gag cat atg cgc acc aac gtc gac ggc atc tac gcc atc ggt gac gtc	1744
Glu His Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val	
300 305 310	
acc gcc aag ctg cag ctg gca cac gtc gcc gag gca cag ggc att gtc	1792
Thr Ala Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val	
315 320 325	
gcc gcc gag aca ctc gcc ggc gca gaa acc cag acc ctg ggc gac tac	1840
Ala Ala Glu Thr Leu Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr	
330 335 340 345	
atg atg atg ccg cgt gcc acc ttc tgc aac cca cag gtt gcc tcc ttc	1888
Met Met Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ala Ser Phe	
350 355 360	
ggt tac acc gag gag cag gcc aag gag aag tgg ccg gat cga gag atc	1936
Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile	
365 370 375	
aag gtg tcc tcc ttc ccg ttc tcc gcg aac ggc aag gcc gtc ggc ctg	1984
Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu	
380 385 390	
gct gag acc gat ggt ttc gcc aag atc gtc gcc gac gct gag ttc ggt	2032
Ala Glu Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly	
395 400 405	
gaa ctg ctg ggt ggc cac att gtc ggt gcc aac gcc tcc gag ctg ctc	2080
Glu Leu Leu Gly Gly His Ile Val Gly Ala Asn Ala Ser Glu Leu Leu	
410 415 420 425	
aac gag ctg gtg ctg gcc cag aac tgg gat ctc acc acc gag gag atc	2128
Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile	
430 435 440	
agc cgc agc gtc cac atc cac ccg acc ctg tcg gag gct gtc aag gaa	2176
Ser Arg Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu	
445 450 455	
gct gcc cac ggc gtc aac ggc cac atg atc aac ttc taaatcccgt	2222
Ala Ala His Gly Val Asn Gly His Met Ile Asn Phe	
460 465	
cagacaaatg caaatcccct caccgatggc atatcggtga ggggattttc tcatgcacgt	2282
aaatcataa tccatggcaa ggaaagtcga caacagcgcc	2322

<210> 32

<211> 469

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 32

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20 25 30	
Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile	
35 40 45	

Pro	Ser	Lys	Ala	Leu	Ile	Lys	Asn	Ala	Glu	Ile	Ala	His	Ile	Phe	Asn
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His	Glu	Lys	Lys	Thr	Phe	Gly	Ile	Asn	Gly	Glu	Val	Thr	Phe	Asn	Tyr
65					70					75					80
Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	Val	Ser	Asp	Lys	Ile	Val	Gly
				85					90					95	
Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile	Thr	Glu	Ile	Asp	Gly
			100					105					110		
Phe	Gly	Thr	Phe	Lys	Asp	Ala	Lys	Thr	Ile	Glu	Val	Thr	Asp	Gly	Lys
		115					120					125			
Asp	Ala	Gly	Lys	Thr	Val	Thr	Phe	Asp	Asp	Cys	Ile	Ile	Ala	Thr	Gly
	130					135					140				
Ser	Val	Val	Asn	Ser	Leu	Arg	Gly	Val	Glu	Phe	Ser	Glu	Asn	Val	Val
145					150					155					160
Ser	Tyr	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala	Pro	Lys	Lys	Met	Val
				165				170						175	
Ile	Val	Gly	Gly	Gly	Ala	Ile	Gly	Met	Glu	Phe	Ala	Tyr	Val	Leu	Gly
			180					185					190		
Asn	Tyr	Gly	Val	Asp	Val	Thr	Leu	Ile	Glu	Phe	Met	Asp	Arg	Val	Leu
		195					200					205			
Pro	Asn	Glu	Asp	Pro	Glu	Val	Ser	Lys	Val	Ile	Ala	Lys	Ala	Tyr	Lys
	210					215					220				
Lys	Met	Gly	Ile	Lys	Leu	Leu	Pro	Gly	His	Ala	Thr	Thr	Ala	Val	Arg
225					230					235					240
Asp	Asn	Gly	Asp	Ser	Val	Glu	Val	Asp	Tyr	Gln	Lys	Lys	Gly	Ser	Asp
				245					250					255	
Lys	Thr	Glu	Thr	Ile	Thr	Val	Asp	Arg	Val	Leu	Ile	Ser	Val	Gly	Phe
			260					265					270		
Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn	Thr	Gly	Val	Lys	Leu
		275					280					285			
Thr	Glu	Arg	Gly	Ala	Ile	Asp	Ile	Asp	Glu	His	Met	Arg	Thr	Asn	Val
	290					295					300				
Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala	Lys	Leu	Gln	Leu	Ala
305					310					315					320
His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala	Glu	Thr	Leu	Ala	Gly
				325					330					335	
Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met	Met	Pro	Arg	Ala	Thr
			340					345					350		
Phe	Cys	Asn	Pro	Gln	Val	Ala	Ser	Phe	Gly	Tyr	Thr	Glu	Glu	Gln	Ala
		355					360					365			
Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val	Ser	Ser	Phe	Pro	Phe
	370					375					380				
Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	Thr	Asp	Gly	Phe	Ala
385					390					395					400
Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	Leu	Gly	Gly	His	Ile
				405					410					415	
Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Leu	Asn	Glu	Leu	Val	Leu	Ala	Gln
			420					425					430		
Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg	Ser	Val	His	Ile	His
		435					440					445			
Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala	His	Gly	Val	Asn	Gly

450
His Met Ile Asn Phe
465

455

460

<210> 33
<211> 4096
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (250)..(3951)

<400> 33

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cgttacagtg	gataaaataa	agcccattta	gaaccctcaa	caagcaagga	aaagaggcga	240
gtacctgcc	gtg agc agc	gct agt act	ttc ggc cag	aac gcg tgg	ctg gtg	291
	Val Ser Ser	Ala Ser Thr	Phe Gly Gln	Asn Ala Trp	Leu Val	
	1	5	10			
gat gag atg	ttc cag cag	ttc aag aag	gac ccc cag	tcc gtg gac	aag	339
Asp Glu Met	Phe Gln Gln	Phe Lys Lys	Asp Pro Gln	Ser Val Asp	Lys	
15	20	25	30			
gaa tgg aga	gag ctc ttc	gag tct cag	ggg ggt ccc	cag gct gaa	aag	387
Glu Trp Arg	Glu Leu Phe	Glu Ser Gln	Gly Gly Pro	Gln Ala Glu	Lys	
	35	40	45			
gct acc ccc	gcc acc ccc	gaa gcc aag	aag gca gct	tcg tcg cag	tcc	435
Ala Thr Pro	Ala Thr Pro	Glu Ala Lys	Lys Ala Ala	Ser Ser Gln	Ser	
	50	55	60			
tca act tcc	gga cag tcc	acc gcc aag	gct gcc cct	gcc gcc aag	acc	483
Ser Thr Ser	Gly Gln Ser	Thr Ala Lys	Ala Ala Pro	Ala Ala Lys	Thr	
	65	70	75			
gca ccg gcc	tct gcg cca	gcc aag gct	gcc cct gtt	aag caa aac	cag	531
Ala Pro Ala	Ser Ala Pro	Ala Lys Ala	Ala Pro Val	Lys Gln Asn	Gln	
	80	85	90			
gcg tcc aag	cct gcc aag	aag gcc aag	gag tcc ccc	ctg tcc aag	cca	579
Ala Ser Lys	Pro Ala Lys	Lys Ala Lys	Glu Ser Pro	Leu Ser Lys	Pro	
	95	100	105			
gct gcc atg	cct gag ccg	gga acc acc	cca ctc agg	ggc atc ttc	aag	627
Ala Ala Met	Pro Glu Pro	Gly Thr Thr	Pro Leu Arg	Gly Ile Phe	Lys	
	115	120	125			
tcc atc gcc	aag aac atg	gac ctc tcc	ctc gag gtg	ccc acc gcc	acc	675
Ser Ile Ala	Lys Asn Met	Asp Leu Ser	Leu Glu Val	Pro Thr Ala	Thr	
	130	135	140			
tcc gtc cgc	gac atg ccc	gcg cgc ctc	atg ttc gag	aac cgc gcc	atg	723
Ser Val Arg	Asp Met Pro	Ala Arg Leu	Met Phe Glu	Asn Arg Ala	Met	
	145	150	155			
gtc aac gac	cag ctc aag	cgc acc cgt	ggc ggc aag	atc tcc ttc	acc	771
Val Asn Asp	Gln Leu Lys	Arg Thr Arg	Gly Gly Lys	Ile Ser Phe	Thr	
	160	165	170			

cac	atc	atc	ggc	tac	gcc	atg	gtg	aag	gct	gtc	atg	gca	cac	ccg	gac	819
His	Ile	Ile	Gly	Tyr	Ala	Met	Val	Lys	Ala	Val	Met	Ala	His	Pro	Asp	
175					180					185					190	
atg	aac	aac	tcc	tat	gac	atc	gtc	gac	ggc	aag	ccg	tcc	ctg	gtc	gtc	867
Met	Asn	Asn	Ser	Tyr	Asp	Ile	Val	Asp	Gly	Lys	Pro	Ser	Leu	Val	Val	
				195					200					205		
ccg	gag	cac	atc	aac	ctc	ggc	ctg	gcc	atc	gac	ctc	ccc	cag	aag	gac	915
Pro	Glu	His	Ile	Asn	Leu	Gly	Leu	Ala	Ile	Asp	Leu	Pro	Gln	Lys	Asp	
			210					215					220			
ggc	tcc	cgt	gcc	ctc	gtg	gtc	gcc	gcc	atc	aag	gaa	acc	gag	aag	atg	963
Gly	Ser	Arg	Ala	Leu	Val	Val	Ala	Ala	Ile	Lys	Glu	Thr	Glu	Lys	Met	
		225					230					235				
acc	ttc	tcc	cag	ttc	ctg	gag	gcc	tat	gag	gac	gtt	gtg	gca	cgc	tcc	1011
Thr	Phe	Ser	Gln	Phe	Leu	Glu	Ala	Tyr	Glu	Asp	Val	Val	Ala	Arg	Ser	
	240				245						250					
cgc	gtc	ggc	aag	ctc	acc	atg	gat	gac	tac	cag	ggt	gtc	acc	atc	tcc	1059
Arg	Val	Gly	Lys	Leu	Thr	Met	Asp	Asp	Tyr	Gln	Gly	Val	Thr	Ile	Ser	
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ttg	acc	aac	ccg	ggt	ggc	atc	ggt	acc	cgc	cac	tcc	atc	ccg	cgt	ctg	1107
Leu	Thr	Asn	Pro	Gly	Gly	Ile	Gly	Thr	Arg	His	Ser	Ile	Pro	Arg	Leu	
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acc	aag	ggc	cag	ggc	acc	atc	atc	ggt	gtc	ggt	tcc	atg	gac	tac	ccg	1155
Thr	Lys	Gly	Gln	Gly	Thr	Ile	Ile	Gly	Val	Gly	Ser	Met	Asp	Tyr	Pro	
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gcc	gag	ttc	cag	ggt	gcc	tcc	gag	gac	cgt	ctc	gcc	gag	ctc	ggt	gtg	1203
Ala	Glu	Phe	Gln	Gly	Ala	Ser	Glu	Asp	Arg	Leu	Ala	Glu	Leu	Gly	Val	
		305					310					315				
ggc	aag	ctc	gtc	acc	atc	acc	tcc	acc	tac	gat	cac	cgc	gtc	atc	cag	1251
Gly	Lys	Leu	Val	Thr	Ile	Thr	Ser	Thr	Tyr	Asp	His	Arg	Val	Ile	Gln	
	320				325						330					
ggc	gcg	gaa	tcc	ggt	gag	ttc	ctg	cgc	acc	atg	tcc	cag	ctg	ctc	gtg	1299
Gly	Ala	Glu	Ser	Gly	Glu	Phe	Leu	Arg	Thr	Met	Ser	Gln	Leu	Leu	Val	
335				340						345					350	
gac	gat	gcg	ttc	tgg	gat	cac	atc	ttc	gag	gag	atg	aac	gtt	ccc	tac	1347
Asp	Asp	Ala	Phe	Trp	Asp	His	Ile	Phe	Glu	Glu	Met	Asn	Val	Pro	Tyr	
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acc	ccg	atg	cgc	tgg	gca	cag	gac	ctg	ccc	aac	acc	ggt	gtg	gac	aag	1395
Thr	Pro	Met	Arg	Trp	Ala	Gln	Asp	Leu	Pro	Asn	Thr	Gly	Val	Asp	Lys	
			370					375					380			
aac	acc	cgt	gtc	atg	cag	ctc	atc	gag	gcc	tac	cgc	tcc	cgc	ggt	cac	1443
Asn	Thr	Arg	Val	Met	Gln	Leu	Ile	Glu	Ala	Tyr	Arg	Ser	Arg	Gly	His	
		385					390					395				
ctc	atc	gcc	gac	acc	aac	cca	ctg	ccc	tgg	gtc	cag	ccc	ggc	atg	ccc	1491
Leu	Ile	Ala	Asp	Thr	Asn	Pro	Leu	Pro	Trp	Val	Gln	Pro	Gly	Met	Pro	
	400				405						410					
gtc	ccg	gat	cac	cgt	gac	ctc	gac	atc	gag	acc	cac	ggc	ctg	acc	ctg	1539
Val	Pro	Asp	His	Arg	Asp	Leu	Asp	Ile	Glu	Thr	His	Gly	Leu	Thr	Leu	
415					420					425					430	
tgg	gat	ctg	gac	cgt	acc	ttc	cac	gtc	ggt	ggt	ttc	ggt	ggc	aag	gag	1587
Trp	Asp	Leu	Asp	Arg	Thr	Phe	His	Val	Gly	Gly	Phe	Gly	Gly	Lys	Glu	
				435					440					445		

acc	atg	acc	ctg	cgc	gag	gtg	ctc	agc	cgc	ctc	cgc	gcc	gcc	tac	acc	1635
Thr	Met	Thr	Leu	Arg	Glu	Val	Leu	Ser	Arg	Leu	Arg	Ala	Ala	Tyr	Thr	
			450					455					460			
ctc	aag	gtc	ggc	tcc	gag	tac	acc	cac	atc	ctc	gac	cgc	gat	gag	cgc	1683
Leu	Lys	Val	Gly	Ser	Glu	Tyr	Thr	His	Ile	Leu	Asp	Arg	Asp	Glu	Arg	
		465					470					475				
acc	tgg	ctg	cag	gac	cgc	ctc	gag	gcc	ggt	atg	ccc	aag	ccc	acc	gcc	1731
Thr	Trp	Leu	Gln	Asp	Arg	Leu	Glu	Ala	Gly	Met	Pro	Lys	Pro	Thr	Ala	
	480					485					490					
gcc	gag	cag	aag	tac	atc	ctg	cag	aag	ctc	aac	gcc	gcc	gag	gca	ttc	1779
Ala	Glu	Gln	Lys	Tyr	Ile	Leu	Gln	Lys	Leu	Asn	Ala	Ala	Glu	Ala	Phe	
495					500					505					510	
gag	aac	ttc	ctg	cag	acc	aag	tac	gtc	ggc	cag	aag	cgt	ttc	tcc	ctc	1827
Glu	Asn	Phe	Leu	Gln	Thr	Lys	Tyr	Val	Gly	Gln	Lys	Arg	Phe	Ser	Leu	
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gag	ggt	gcc	gag	tca	ctg	atc	ccg	ctg	atg	gac	tcc	gcc	atc	gac	acc	1875
Glu	Gly	Ala	Glu	Ser	Leu	Ile	Pro	Leu	Met	Asp	Ser	Ala	Ile	Asp	Thr	
			530					535					540			
gcc	gca	ggc	cag	ggc	ctt	gac	gag	gtc	gtc	atc	ggc	atg	ccc	cac	cgt	1923
Ala	Ala	Gly	Gln	Gly	Leu	Asp	Glu	Val	Val	Ile	Gly	Met	Pro	His	Arg	
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ggt	cgc	ctc	aac	gtg	ctg	ttc	aac	atc	gtc	ggc	aag	cca	ctg	gcc	tcg	1971
Gly	Arg	Leu	Asn	Val	Leu	Phe	Asn	Ile	Val	Gly	Lys	Pro	Leu	Ala	Ser	
	560					565					570					
atc	ttc	aac	gag	ttc	gag	ggc	cag	atg	gag	cag	ggc	cag	atc	ggt	ggc	2019
Ile	Phe	Asn	Glu	Phe	Glu	Gly	Gln	Met	Glu	Gln	Gly	Gln	Ile	Gly	Gly	
575					580					585					590	
tcc	ggt	gac	gtg	aag	tac	cac	ctc	ggt	tcc	gag	ggc	acc	cac	ctg	cag	2067
Ser	Gly	Asp	Val	Lys	Tyr	His	Leu	Gly	Ser	Glu	Gly	Thr	His	Leu	Gln	
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Met	Phe	Gly	Asp	Gly	Glu	Ile	Lys	Val	Ser	Leu	Thr	Ala	Asn	Pro	Ser	
			610					615					620			
cac	ctc	gag	gcc	gtc	aac	ccg	gtc	gtg	gag	ggc	atc	gtc	cgc	gcc	aag	2163
His	Leu	Glu	Ala	Val	Asn	Pro	Val	Val	Glu	Gly	Ile	Val	Arg	Ala	Lys	
		625					630					635				
cag	gac	atc	ctg	gac	aag	ggc	ccg	gac	ggc	tac	acc	gtc	gtc	ccg	ctg	2211
Gln	Asp	Ile	Leu	Asp	Lys	Gly	Pro	Asp	Gly	Tyr	Thr	Val	Val	Pro	Leu	
	640					645					650					
ctg	ctc	cac	ggt	gac	gcc	gcc	ttc	gcc	ggc	ctg	ggc	atc	gtg	ccc	gag	2259
Leu	Leu	His	Gly	Asp	Ala	Ala	Phe	Ala	Gly	Leu	Gly	Ile	Val	Pro	Glu	
655					660					665					670	
acc	atc	aac	ctc	gca	gcc	ctg	cgt	ggt	tac	gat	gtc	ggt	ggc	acc	atc	2307
Thr	Ile	Asn	Leu	Ala	Ala	Leu	Arg	Gly	Tyr	Asp	Val	Gly	Gly	Thr	Ile	
			675					680						685		
cac	atc	gtg	gtc	aac	aac	cag	atc	ggc	ttc	acc	acc	acc	ccg	gac	tcc	2355
His	Ile	Val	Val	Asn	Asn	Gln	Ile	Gly	Phe	Thr	Thr	Thr	Pro	Asp	Ser	
			690					695					700			
agc	cgt	tcc	atg	cac	tac	gcc	acc	gac	tgc	gcc	aag	gcc	ttc	ggt	tgc	2403
Ser	Arg	Ser	Met	His	Tyr	Ala	Thr	Asp	Cys	Ala	Lys	Ala	Phe	Gly	Cys	
		705					710					715				

ccg	gtg	ttc	cac	gtc	aac	ggt	gac	gac	ccc	gag	gct	gtg	gtc	tgg	gtc	2451
Pro	Val	Phe	His	Val	Asn	Gly	Asp	Asp	Pro	Glu	Ala	Val	Val	Trp	Val	
720						725					730					
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Gly	Gln	Leu	Ala	Thr	Glu	Tyr	Arg	Arg	Arg	Phe	Gly	Lys	Asp	Val	Phe	
735					740					745					750	
atc	gac	ctc	atc	tgc	tac	cgc	ctg	cgc	ggc	cac	aac	gag	gct	gat	gac	2547
Ile	Asp	Leu	Ile	Cys	Tyr	Arg	Leu	Arg	Gly	His	Asn	Glu	Ala	Asp	Asp	
				755					760					765		
cca	tcc	atg	acc	cag	ccg	aag	atg	tac	gag	ctg	atc	acc	ggc	cgc	gac	2595
Pro	Ser	Met	Thr	Gln	Pro	Lys	Met	Tyr	Glu	Leu	Ile	Thr	Gly	Arg	Asp	
			770					775					780			
tcc	gtg	cgt	gcc	acc	tac	acc	gag	gac	ctc	ctc	ggc	cgt	ggg	gac	ctc	2643
Ser	Val	Arg	Ala	Thr	Tyr	Thr	Glu	Asp	Leu	Leu	Gly	Arg	Gly	Asp	Leu	
		785					790					795				
tcc	ccc	gag	gac	gcc	gag	gcc	gtt	gtc	cgc	gac	ttc	cac	gac	cag	atg	2691
Ser	Pro	Glu	Asp	Ala	Glu	Ala	Val	Val	Arg	Asp	Phe	His	Asp	Gln	Met	
	800					805					810					
gaa	tcc	gtg	ttc	aac	gag	gtc	aag	gaa	gcc	ggc	aag	aag	cag	cct	gat	2739
Glu	Ser	Val	Phe	Asn	Glu	Val	Lys	Glu	Ala	Gly	Lys	Lys	Gln	Pro	Asp	
815					820					825					830	
gag	cag	acc	ggc	atc	acc	ggt	tcc	cag	gaa	ctg	acc	cgt	ggc	ctg	gac	2787
Glu	Gln	Thr	Gly	Ile	Thr	Gly	Ser	Gln	Glu	Leu	Thr	Arg	Gly	Leu	Asp	
			835						840					845		
acc	aac	atc	acc	cgc	gag	gaa	ctg	gtc	gaa	ctc	ggc	cag	gcc	ttc	gtc	2835
Thr	Asn	Ile	Thr	Arg	Glu	Glu	Leu	Val	Glu	Leu	Gly	Gln	Ala	Phe	Val	
			850					855					860			
aac	acc	cca	gag	ggc	ttc	acc	tac	cac	cca	cgt	gtg	gca	ccg	gtg	gcc	2883
Asn	Thr	Pro	Glu	Gly	Phe	Thr	Tyr	His	Pro	Arg	Val	Ala	Pro	Val	Ala	
		865					870					875				
aag	aag	cgt	gcc	gag	tcc	gtc	acc	gag	ggt	ggc	atc	gac	tgg	gca	tgg	2931
Lys	Lys	Arg	Ala	Glu	Ser	Val	Thr	Glu	Gly	Gly	Ile	Asp	Trp	Ala	Trp	
	880					885					890					
ggc	gag	ctc	atc	gcc	ttc	ggc	tcc	ctg	gcc	acc	tcc	ggc	agg	ctg	gtc	2979
Gly	Glu	Leu	Ile	Ala	Phe	Gly	Ser	Leu	Ala	Thr	Ser	Gly	Arg	Leu	Val	
895					900					905					910	
cgc	ctc	gcc	ggt	gag	gat	tcc	cgc	cgt	ggt	acc	ttc	acc	cag	cgt	cac	3027
Arg	Leu	Ala	Gly	Glu	Asp	Ser	Arg	Arg	Gly	Thr	Phe	Thr	Gln	Arg	His	
			915						920					925		
gcc	gtg	gcc	atc	gac	ccg	aac	acc	gcc	gag	gag	ttc	aac	ccg	ctc	cac	3075
Ala	Val	Ala	Ile	Asp	Pro	Asn	Thr	Ala	Glu	Glu	Phe	Asn	Pro	Leu	His	
			930					935					940			
gag	ctg	gca	cag	gcc	aag	ggc	ggc	ggc	aag	ttc	ctc	gtc	tac	aac	tcc	3123
Glu	Leu	Ala	Gln	Ala	Lys	Gly	Gly	Gly	Lys	Phe	Leu	Val	Tyr	Asn	Ser	
		945					950					955				
gcg	ctg	acc	gag	tac	gcg	ggt	atg	ggc	ttc	gaa	tac	ggc	tac	tcc	gtg	3171
Ala	Leu	Thr	Glu	Tyr	Ala	Gly	Met	Gly	Phe	Glu	Tyr	Gly	Tyr	Ser	Val	
	960					965					970					
ggc	aac	ccg	gac	gcc	gtg	gtg	tcc	tgg	gag	gca	cag	ttc	ggt	gac	ttc	3219
Gly	Asn	Pro	Asp	Ala	Val	Val	Ser	Trp	Glu	Ala	Gln	Phe	Gly	Asp	Phe	
975					980					985					990	

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Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu	
995 1000 1005	
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Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly	
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Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe	
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ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc	3411
Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr	
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ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg	3459
Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met	
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aag cgc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag	3507
Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys	
1075 1080 1085	
gcc gcc acc tcc gct ccg gag gag ttc acc gag gtc acc cgc ttc aag	3555
Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys	
1090 1095 1100	
tcc gtg atc gac gat ccg aac gtg gcg gat gcc tcc aag gtg aag aag	3603
Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys	
1105 1110 1115	
atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag	3651
Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys	
1120 1125 1130	
gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg	3699
Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu	
1135 1140 1145 1150	
cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac ggc tac ccc	3747
His Pro Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro	
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aac gcc gag gag atc ctg ttc gtt cag gac gag ccg gca aac cag ggt	3795
Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly	
1170 1175 1180	
gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctc atc gag ggc atg	3843
Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met	
1185 1190 1195	
ctc ccg atg cgt cgc atc tcg cgc cgt tcc cag tcc tcg act gcg acc	3891
Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr	
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ggt atc gcg aag gtg cac acc atc gag cag cag aag ctg ctg gat gat	3939
Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp	
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<400> 34

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		35					40					45			
Pro	Ala	Thr	Pro	Glu	Ala	Lys	Lys	Ala	Ala	Ser	Ser	Gln	Ser	Ser	Thr
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65					70				75						80
Ala	Ser	Ala	Pro	Ala	Lys	Ala	Ala	Pro	Val	Lys	Gln	Asn	Gln	Ala	Ser
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Lys	Pro	Ala	Lys	Lys	Ala	Lys	Glu	Ser	Pro	Leu	Ser	Lys	Pro	Ala	Ala
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Met	Pro	Glu	Pro	Gly	Thr	Thr	Pro	Leu	Arg	Gly	Ile	Phe	Lys	Ser	Ile
		115					120					125			
Ala	Lys	Asn	Met	Asp	Leu	Ser	Leu	Glu	Val	Pro	Thr	Ala	Thr	Ser	Val
	130					135					140				
Arg	Asp	Met	Pro	Ala	Arg	Leu	Met	Phe	Glu	Asn	Arg	Ala	Met	Val	Asn
145					150					155					160
Asp	Gln	Leu	Lys	Arg	Thr	Arg	Gly	Gly	Lys	Ile	Ser	Phe	Thr	His	Ile
				165					170					175	
Ile	Gly	Tyr	Ala	Met	Val	Lys	Ala	Val	Met	Ala	His	Pro	Asp	Met	Asn
			180					185					190		
Asn	Ser	Tyr	Asp	Ile	Val	Asp	Gly	Lys	Pro	Ser	Leu	Val	Val	Pro	Glu
		195					200					205			
His	Ile	Asn	Leu	Gly	Leu	Ala	Ile	Asp	Leu	Pro	Gln	Lys	Asp	Gly	Ser
	210					215					220				
Arg	Ala	Leu	Val	Val	Ala	Ala	Ile	Lys	Glu	Thr	Glu	Lys	Met	Thr	Phe
225					230					235					240
Ser	Gln	Phe	Leu	Glu	Ala	Tyr	Glu	Asp	Val	Val	Ala	Arg	Ser	Arg	Val
				245					250					255	
Gly	Lys	Leu	Thr	Met	Asp	Asp	Tyr	Gln	Gly	Val	Thr	Ile	Ser	Leu	Thr
			260					265						270	
Asn	Pro	Gly	Gly	Ile	Gly	Thr	Arg	His	Ser	Ile	Pro	Arg	Leu	Thr	Lys
		275					280					285			
Gly	Gln	Gly	Thr	Ile	Ile	Gly	Val	Gly	Ser	Met	Asp	Tyr	Pro	Ala	Glu
	290					295					300				
Phe	Gln	Gly	Ala	Ser	Glu	Asp	Arg	Leu	Ala	Glu	Leu	Gly	Val	Gly	Lys
305					310					315					320
Leu	Val	Thr	Ile	Thr	Ser	Thr	Tyr	Asp	His	Arg	Val	Ile	Gln	Gly	Ala
				325					330					335	
Glu	Ser	Gly	Glu	Phe	Leu	Arg	Thr	Met	Ser	Gln	Leu	Leu	Val	Asp	Asp
			340					345					350		
Ala	Phe	Trp	Asp	His	Ile	Phe	Glu	Glu	Met	Asn	Val	Pro	Tyr	Thr	Pro
		355					360					365			

Met	Arg	Trp	Ala	Gln	Asp	Leu	Pro	Asn	Thr	Gly	Val	Asp	Lys	Asn	Thr
	370					375					380				
Arg	Val	Met	Gln	Leu	Ile	Glu	Ala	Tyr	Arg	Ser	Arg	Gly	His	Leu	Ile
385					390					395					400
Ala	Asp	Thr	Asn	Pro	Leu	Pro	Trp	Val	Gln	Pro	Gly	Met	Pro	Val	Pro
				405					410					415	
Asp	His	Arg	Asp	Leu	Asp	Ile	Glu	Thr	His	Gly	Leu	Thr	Leu	Trp	Asp
			420					425					430		
Leu	Asp	Arg	Thr	Phe	His	Val	Gly	Gly	Phe	Gly	Gly	Lys	Glu	Thr	Met
	435						440					445			
Thr	Leu	Arg	Glu	Val	Leu	Ser	Arg	Leu	Arg	Ala	Ala	Tyr	Thr	Leu	Lys
	450					455					460				
Val	Gly	Ser	Glu	Tyr	Thr	His	Ile	Leu	Asp	Arg	Asp	Glu	Arg	Thr	Trp
465					470					475					480
Leu	Gln	Asp	Arg	Leu	Glu	Ala	Gly	Met	Pro	Lys	Pro	Thr	Ala	Ala	Glu
				485					490					495	
Gln	Lys	Tyr	Ile	Leu	Gln	Lys	Leu	Asn	Ala	Ala	Glu	Ala	Phe	Glu	Asn
			500					505					510		
Phe	Leu	Gln	Thr	Lys	Tyr	Val	Gly	Gln	Lys	Arg	Phe	Ser	Leu	Glu	Gly
	515						520					525			
Ala	Glu	Ser	Leu	Ile	Pro	Leu	Met	Asp	Ser	Ala	Ile	Asp	Thr	Ala	Ala
	530					535					540				
Gly	Gln	Gly	Leu	Asp	Glu	Val	Val	Ile	Gly	Met	Pro	His	Arg	Gly	Arg
545					550					555					560
Leu	Asn	Val	Leu	Phe	Asn	Ile	Val	Gly	Lys	Pro	Leu	Ala	Ser	Ile	Phe
				565					570					575	
Asn	Glu	Phe	Glu	Gly	Gln	Met	Glu	Gln	Gly	Gln	Ile	Gly	Gly	Ser	Gly
			580					585					590		
Asp	Val	Lys	Tyr	His	Leu	Gly	Ser	Glu	Gly	Thr	His	Leu	Gln	Met	Phe
		595					600					605			
Gly	Asp	Gly	Glu	Ile	Lys	Val	Ser	Leu	Thr	Ala	Asn	Pro	Ser	His	Leu
	610					615					620				
Glu	Ala	Val	Asn	Pro	Val	Val	Glu	Gly	Ile	Val	Arg	Ala	Lys	Gln	Asp
625					630					635					640
Ile	Leu	Asp	Lys	Gly	Pro	Asp	Gly	Tyr	Thr	Val	Val	Pro	Leu	Leu	Leu
				645					650					655	
His	Gly	Asp	Ala	Ala	Phe	Ala	Gly	Leu	Gly	Ile	Val	Pro	Glu	Thr	Ile
			660				665						670		
Asn	Leu	Ala	Ala	Leu	Arg	Gly	Tyr	Asp	Val	Gly	Gly	Thr	Ile	His	Ile
		675					680					685			
Val	Val	Asn	Asn	Gln	Ile	Gly	Phe	Thr	Thr	Thr	Pro	Asp	Ser	Ser	Arg
	690					695					700				
Ser	Met	His	Tyr	Ala	Thr	Asp	Cys	Ala	Lys	Ala	Phe	Gly	Cys	Pro	Val
705					710					715					720
Phe	His	Val	Asn	Gly	Asp	Asp	Pro	Glu	Ala	Val	Val	Trp	Val	Gly	Gln
				725					730					735	
Leu	Ala	Thr	Glu	Tyr	Arg	Arg	Arg	Phe	Gly	Lys	Asp	Val	Phe	Ile	Asp
			740					745					750		
Leu	Ile	Cys	Tyr	Arg	Leu	Arg	Gly	His	Asn	Glu	Ala	Asp	Asp	Pro	Ser
		755					760					765			
Met	Thr	Gln	Pro	Lys	Met	Tyr	Glu	Leu	Ile	Thr	Gly	Arg	Asp	Ser	Val

770	775	780
Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu Ser Pro		
785	790	795
Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met Glu Ser		
	805	810
Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp Glu Gln		
	820	825
Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp Thr Asn		
	835	840
Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val Asn Thr		
	850	855
Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala Lys Lys		
865	870	875
Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp Gly Glu		
	885	890
Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val Arg Leu		
	900	905
Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His Ala Val		
	915	920
Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His Glu Leu		
	930	935
Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu		
945	950	955
Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn		
	965	970
Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn		
	980	985
Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu Ala Lys		
	995	1000
Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly Tyr Glu		
	1010	1015
Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln		
1025	1030	1035
Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr Pro Ala		
	1045	1050
Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met Lys Arg		
	1060	1065
Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys Ala Ala		
	1075	1080
Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys Ser Val		
	1090	1095
Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys Ile Met		
1105	1110	1115
Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys		
	1125	1130
Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu His Pro		
	1140	1145
Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala		
	1155	1160
Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp		
	1170	1175
		1180

Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro
 1185 1190 1195 1200
 Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile
 1205 1210 1215
 Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe
 1220 1225 1230
 Asn Ala

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for aceA

<400> 35
 cctctaccca gcgaactccg 20

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for aceA

<400> 36
 ctgccttgaa ctcacggttc 20

<210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for accBC

<400> 37
 catccacccc ggctacggct 20

<210> 38
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for accBC

<400> 38
 cggtgactgg gtgttccacc 20

<210> 39
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for dtsR1

 <400> 39
 acggcccagc cctgaccgac 20

 <210> 40
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for dtsR1

 <400> 40
 agcagcgccc atgacggcga 20

 <210> 41
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for dtsR2

 <400> 41
 acggcccagc cctgaccgac 20

 <210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for dtsR2

 <400> 42
 agcagcgccc atgacggcga 20

 <210> 43
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: primer for pfk

<400> 43

cgtcatccga ggaatcgtcc

20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pfk

<400> 44

cgtggcggcc catgacctcc

20

<210> 45

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for scrB

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<222> (3)..(3)

<223> n = a, c, g, or t

<400> 45

ggncghytba aygaycc

17

<210> 46

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: primer for scrB

<220>

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<222> (18)..(18)

<223> n = a, c, g, or t

<400> 46

ggrcaytccc acatrtancc

20

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 47

ccatccggat ccggcaagtc

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 48

aatcccatct cgtgggtaac

20

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 49

actgtgtcca tgggtcttgg ccc

23

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 50

cgctggaatccgaacatcga

20

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 51

ggcgcaacct acgacgttgc aatgcg

26

<210> 52
 <211> 20
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 <400> 52
 tggccgcctg ggatctcgtg 20

 <210> 53
 <211> 20
 <212> DNA
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 <400> 53
 gggtcctgga ttggtggaga 20

 <210> 54
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for ppc

 <400> 54
 ccgccatcct tggttggaatc 20

 <210> 55
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for acn

 <220>
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 <223> n = inosine

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 <400> 55
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 <210> 56
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 <212> DNA
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 <223> n = inosine

 <400> 56
 gcnggagana tgtgrtcngt 20

 <210> 57
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for icd

 <400> 57
 gacatttcac tcgctggacg 20

 <210> 58
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for icd

 <400> 58
 ccgtactctt cagccttctg 20

 <210> 59
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for lpd

 <400> 59
 atcatcgcaa ccggttc 17

 <210> 60
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for lpd

 <400> 60
 cgtcaccgat ggcgtaaatt 19

 <210> 61
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for odhA

 <400> 61
 acaccgtggt cgcctcaacg 20

 <210> 62
 <211> 20
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: primer for odhA

 <400> 62
 tgctaaccg tcccacctgg 20

 <210> 63

<211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 screening PCR of lpd

 <400> 63
 tacgaggagc agatcctcaa 20

 <210> 64
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 screening PCR of lpd

 <400> 64
 ttgacgccgg tggttctccag 20

 <210> 65
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of acn

 <400> 65
 ggtgaagcta agtagttagc 20

 <210> 66
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of acn

 <400> 66
 agctactaaa cctgcacc 18

 <210> 67
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of icd

 <400> 67
 ccgtactctt cagccttctg 20

 <210> 68
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of icd

 <400> 68
 tcgtccttgt tccacatc 18

 <210> 69
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of lpd

 <400> 69
 atcatcgcaa ccggttc 17

 <210> 70
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of lpd

 <400> 70
 tacgaggagc agatcctcaa 20

 <210> 71
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for

LA cloning of acn

<400> 71
gctaactact tagcttcacc 20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 72
gaaccaggaa ctattgaacc 20

<210> 73
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 73
tccgatgtca tcatcgac 18

<210> 74
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 74
atgtggaaca aggacgac 18

<210> 75
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 75

gtacatattg tcgttagaac gcgtaatacg actca 35

<210> 76
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of odhA

<400> 76
 cgtagaacg cgtaatacga ctactatag ggaga 35

<210> 77
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying gdh gene

<400> 77
 gcgcctgcag gtccgagggt gtgcgttcgg ca 32

<210> 78
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying gdh gene

<400> 78
 gcgcctgcag ccaccagga tgccctcaacc ag 32

<210> 79
 <211> 1344
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (1)..(1341)

<400> 79

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Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
1				5					10					15		
cgc	aac	gcc	ggg	gaa	cct	gag	ttc	cac	cag	gct	gtc	gcg	gag	gtt	ctc	96
Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
			20					25					30			
gaa	tct	ctg	aag	atc	gtc	ctg	gag	aag	gac	ccg	cac	tac	gcc	gac	tac	144
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
		35					40					45				
ggg	ctg	atc	cag	cgt	ctc	tgc	gaa	ccg	gaa	cgc	cag	ctg	atc	ttc	cgt	192
Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
	50					55					60					
gtg	ccc	tgg	gtg	gat	gac	aac	ggg	cag	gtg	cac	gtc	aac	cgt	ggg	ttc	240
Val	Pro	Trp	Val	Asp	Asp	Asn	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
65					70					75					80	
cgt	gtc	cag	ttc	aac	tcc	gca	ctc	ggc	ccg	tac	aag	ggg	ggg	ctg	cgt	288
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	
				85					90					95		
ttc	cac	ccc	tcc	gtc	aac	ctc	ggc	atc	gtc	aag	ttc	ctc	ggc	ttc	gag	336
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	
			100					105					110			
cag	atc	ttc	aag	aac	tcc	ctc	acc	ggg	ctg	ccg	atc	ggg	ggc	ggc	aag	384
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys	
		115					120					125				
ggg	ggg	tcc	gac	ttc	gac	ccg	aag	ggc	aag	tcc	gag	ctg	gag	atc	atg	432
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Leu	Glu	Ile	Met	
	130					135					140					
cgc	ttc	tgc	cag	tcc	ttc	atg	acc	gag	ctg	cac	cgc	cac	atc	ggc	gag	480
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	
145					150					155					160	
tac	cgg	gat	gtc	ccg	gcc	ggg	gac	atc	gga	gtc	ggg	ggc	cgc	gag	atc	528
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile	
				165					170					175		
ggg	tac	ctc	ttc	ggc	cac	tac	cgc	cgt	ctg	gcc	aac	cag	cac	gag	tcc	576
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Leu	Ala	Asn	Gln	His	Glu	Ser	
			180					185					190			
ggg	gtg	ctc	acc	ggc	aag	ggc	ctg	acc	tgg	ggg	ggg	tcc	ctg	gtc	cgc	624
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	
		195					200					205				
acc	gag	gcc	acc	ggc	ttc	ggc	acc	gtc	tac	ttc	gtc	cag	gag	atg	atc	672
Thr	Glu	Ala	Thr	Gly	Phe	Gly	Thr	Val	Tyr	Phe	Val	Gln	Glu	Met	Ile	
	210					215					220					
aag	gcg	gaa	ggg	gag	acc	ctc	gag	ggc	aag	aag	gtc	atc	gtc	tcc	ggg	720
Lys	Ala	Glu	Gly	Glu	Thr	Leu	Glu	Gly	Lys	Lys	Val	Ile	Val	Ser	Gly	
225					230					235					240	
tcc	ggc	aac	gtg	gcc	acc	tac	gcc	atc	cag	aag	gtg	cag	gaa	ctg	ggg	768
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Gly	
				245					250					255		
gcg	gtt	gtg	gtc	ggc	ttc	tcc	gac	tcc	agc	ggc	tgg	gtc	tcc	acc	ccg	816
Ala	Val	Val	Val	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	Ser	Thr	Pro	
			260					265					270			

aac	ggt	gtt	gac	gtg	gcc	aag	ctg	cgt	gag	atc	aag	gag	gtc	cgt	cgt	864
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	
	275						280					285				
gca	cgc	gtg	tcc	tcc	tac	gcc	gac	gag	gtg	gag	ggt	gcg	gag	tac	cac	912
Ala	Arg	Val	Ser	Ser	Tyr	Ala	Asp	Glu	Val	Glu	Gly	Ala	Glu	Tyr	His	
	290						295					300				
acc	gac	ggc	tcc	atc	tgg	gat	ctg	acc	gcc	gac	atc	gcg	ctg	ccc	tgc	960
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Thr	Ala	Asp	Ile	Ala	Leu	Pro	Cys	
	305				310					315					320	
gcc	acc	cag	aac	gaa	ctg	gac	ggc	gac	aac	gcc	cgc	acc	ctc	gcg	gac	1008
Ala	Thr	Gln	Asn	Glu	Leu	Asp	Gly	Asp	Asn	Ala	Arg	Thr	Leu	Ala	Asp	
				325						330				335		
aac	ggc	tgc	cgc	ttc	gtg	gcg	gag	ggc	gcc	aac	atg	ccc	tcc	acc	ccc	1056
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro	
			340					345					350			
gag	gcc	atc	gac	gtc	ttc	cgt	gag	cgt	ggt	gtt	ctc	ttc	ggg	ccg	ggc	1104
Glu	Ala	Ile	Asp	Val	Phe	Arg	Glu	Arg	Gly	Val	Leu	Phe	Gly	Pro	Gly	
		355					360					365				
aag	gct	gcc	aac	gcc	ggt	ggc	gtg	gcc	acc	tcc	gcc	ctg	gag	atg	cag	1152
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln	
	370					375					380					
cag	aac	gcc	tcc	cgt	gat	tcc	tgg	agc	ttc	gag	tac	acc	gat	gag	cgt	1200
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg	
	385				390					395					400	
ctc	cac	cgc	atc	atg	aag	aac	atc	ttc	aag	tcc	tgc	gcc	gat	acc	gcc	1248
Leu	His	Arg	Ile	Met	Lys	Asn	Ile	Phe	Lys	Ser	Cys	Ala	Asp	Thr	Ala	
				405					410					415		
aag	gag	tac	ggc	cac	gag	aag	aac	tac	gtg	gtc	ggt	gcg	aac	atc	gcc	1296
Lys	Glu	Tyr	Gly	His	Glu	Lys	Asn	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala	
			420					425					430			
gga	ttc	aag	aag	gtc	gct	gac	gcc	atg	ctc	gcc	cag	ggt	gtc	atc	taa	1344
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile		
		435					440					445				

<210> 80

<211> 447

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 80

Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
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Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
			20					25					30			
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
		35					40				45					
Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
	50					55					60					
Val	Pro	Trp	Val	Asp	Asp	Asn	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
	65				70					75					80	
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	

				85					90					95	
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu
			100					105					110		
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys
		115					120					125			
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Leu	Glu	Ile	Met
		130				135					140				
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu
145					150					155					160
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile
				165					170					175	
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Leu	Ala	Asn	Gln	His	Glu	Ser
			180				185					190			
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg
		195					200					205			
Thr	Glu	Ala	Thr	Gly	Phe	Gly	Thr	Val	Tyr	Phe	Val	Gln	Glu	Met	Ile
	210					215					220				
Lys	Ala	Glu	Gly	Glu	Thr	Leu	Glu	Gly	Lys	Lys	Val	Ile	Val	Ser	Gly
225					230					235					240
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Gly
				245					250					255	
Ala	Val	Val	Val	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	Ser	Thr	Pro
			260				265						270		
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg
		275					280					285			
Ala	Arg	Val	Ser	Ser	Tyr	Ala	Asp	Glu	Val	Glu	Gly	Ala	Glu	Tyr	His
	290					295					300				
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Thr	Ala	Asp	Ile	Ala	Leu	Pro	Cys
305					310					315					320
Ala	Thr	Gln	Asn	Glu	Leu	Asp	Gly	Asp	Asn	Ala	Arg	Thr	Leu	Ala	Asp
				325					330					335	
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro
			340					345					350		
Glu	Ala	Ile	Asp	Val	Phe	Arg	Glu	Arg	Gly	Val	Leu	Phe	Gly	Pro	Gly
		355					360					365			
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln
	370					375					380				
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg
385					390					395					400
Leu	His	Arg	Ile	Met	Lys	Asn	Ile	Phe	Lys	Ser	Cys	Ala	Asp	Thr	Ala
				405					410					415	
Lys	Glu	Tyr	Gly	His	Glu	Lys	Asn	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala
			420				425						430		
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile	
		435					440					445			

<210> 81

<211> 1344

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1341)

<400> 81

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Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
1				5					10					15		
cgc	aat	gct	ggc	gag	cct	gaa	ttt	cac	cag	gca	gtg	gca	gag	gtt	ttg	96
Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
			20					25					30			
gaa	tct	ttg	aag	atc	gtc	ctg	gaa	aag	gac	cct	cat	tac	gct	gat	tac	144
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
		35				40						45				
ggt	ctc	atc	cag	cgc	ctg	tgc	gag	cct	gag	cgt	cag	ctc	atc	ttc	cgt	192
Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
	50					55					60					
gtg	cct	tgg	gtt	gat	gac	cag	ggc	cag	gtc	cac	gtc	aac	cgt	ggt	ttc	240
Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
65				70					75						80	
cgc	gtg	cag	ttc	aac	tct	gca	ctt	gga	cca	tac	aag	ggc	ggc	ctg	cgc	288
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	
				85				90						95		
ttc	cac	cca	tct	gta	aac	ctg	ggc	att	gtg	aag	ttc	ctg	ggc	ttt	gag	336
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	
			100					105					110			
cag	atc	ttt	aaa	aac	tcc	cta	acc	ggc	ctg	cca	atc	ggt	ggt	ggc	aag	384
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys	
		115				120						125				
ggt	gga	tcc	gac	ttc	gac	cct	aag	ggc	aag	tcc	gat	ctg	gaa	atc	atg	432
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met	
	130					135					140					
cgt	ttc	tgc	cag	tcc	ttc	atg	acc	gag	ctg	cac	cgc	cac	atc	ggt	gag	480
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	
145					150					155					160	
tac	cgc	gac	gtt	cct	gca	ggt	gac	atc	gga	gtt	ggt	ggc	cgc	gag	atc	528
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile	
				165					170					175		
ggt	tac	ctg	ttt	ggc	cac	tac	cgt	cgc	atg	gct	aac	cag	cac	gag	tcc	576
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser	
			180					185					190			
ggc	gtt	ttg	acc	ggt	aag	ggc	ctg	acc	tgg	ggt	gga	tcc	ctg	gtc	cgc	624
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	
		195					200					205				
acc	gag	gca	act	ggc	tac	ggc	tgc	gtt	tac	ttc	gtg	agt	gaa	atg	atc	672
Thr	Glu	Ala	Thr	Gly	Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile	
	210					215					220					
aag	gct	aag	ggc	gag	agc	atc	agc	ggc	cag	aag	atc	atc	gtt	tcc	ggt	720
Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly	
225					230					235					240	
tcc	ggc	aac	gta	gca	acc	tac	gcg	att	gaa	aag	gct	cag	gaa	ctc	ggc	768

Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly	
				245					250					255		
gca	acc	gtt	att	ggt	ttc	tcc	gat	tcc	agc	ggt	tgg	gtt	cat	acc	cct	816
Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro	
			260				265						270			
aac	ggc	gtt	gac	gtg	gct	aag	ctc	cgc	gaa	atc	aag	gaa	gtt	cgc	cgc	864
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	
		275					280					285				
gca	cgc	gta	tcc	gtg	tac	gcc	gac	gaa	att	gaa	ggc	gca	acc	tac	cac	912
Ala	Arg	Val	Ser	Val	Tyr	Ala	Asp	Glu	Ile	Glu	Gly	Ala	Thr	Tyr	His	
	290					295					300					
acc	gac	ggt	tcc	atc	tgg	gat	ctc	aag	tgc	gat	atc	gct	ctt	cct	tgt	960
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Lys	Cys	Asp	Ile	Ala	Leu	Pro	Cys	
305					310				315						320	
gca	act	cag	aac	gag	ctc	aac	ggc	gag	aac	gct	aag	act	ctt	gca	gac	1008
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Gly	Glu	Asn	Ala	Lys	Thr	Leu	Ala	Asp	
			325					330						335		
aac	ggc	tgc	cgt	ttc	gtt	gct	gaa	ggc	gcg	aac	atg	cct	tcc	acc	cct	1056
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro	
			340					345				350				
gag	gct	gtt	gag	gtc	ttc	cgt	gag	cgc	gac	atc	cgc	ttc	gga	cca	ggc	1104
Glu	Ala	Val	Glu	Val	Phe	Arg	Glu	Arg	Asp	Ile	Arg	Phe	Gly	Pro	Gly	
		355					360					365				
aag	gca	gct	aac	gct	ggt	ggc	gtt	gca	acc	tcc	gct	ctg	gag	atg	cag	1152
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln	
	370				375						380					
cag	aac	gct	tcg	cgc	gat	tcc	tgg	agc	ttc	gag	tac	acc	gac	gag	cgc	1200
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg	
385					390				395						400	
ctc	cag	gtg	atc	atg	aag	aac	atc	ttc	aag	acc	tgt	gca	gag	acc	gca	1248
Leu	Gln	Val	Ile	Met	Lys	Asn	Ile	Phe	Lys	Thr	Cys	Ala	Glu	Thr	Ala	
				405				410						415		
gca	gag	tat	gga	cac	gag	aac	gat	tac	gtt	gtc	ggc	gct	aac	att	gct	1296
Ala	Glu	Tyr	Gly	His	Glu	Asn	Asp	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala	
			420				425					430				
ggc	ttt	aag	aag	gta	gct	gac	gcg	atg	ctg	gca	cag	ggc	gtc	atc	taa	1344
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile		
		435					440					445				

<210> 82

<211> 447

<212> PRT

<213> Brevibacterium lactofermentum

<400> 82

Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
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Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
			20					25					30			
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
		35					40					45				

Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg
	50					55					60				
Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe
65					70					75					80
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg
				85					90					95	
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu
			100					105					110		
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys
		115					120					125			
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met
	130					135					140				
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu
145					150					155					160
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile
			165						170					175	
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser
			180					185					190		
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg
		195					200					205			
Thr	Glu	Ala	Thr	Gly	Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile
	210					215					220				
Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly
225					230					235					240
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly
				245					250					255	
Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro
			260					265					270		
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg
		275					280					285			
Ala	Arg	Val	Ser	Val	Tyr	Ala	Asp	Glu	Ile	Glu	Gly	Ala	Thr	Tyr	His
	290					295					300				
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Lys	Cys	Asp	Ile	Ala	Leu	Pro	Cys
305					310					315					320
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Gly	Glu	Asn	Ala	Lys	Thr	Leu	Ala	Asp
				325					330					335	
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro
			340					345					350		
Glu	Ala	Val	Glu	Val	Phe	Arg	Glu	Arg	Asp	Ile	Arg	Phe	Gly	Pro	Gly
		355					360					365			
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln
	370					375					380				
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg
385					390					395					400
Leu	Gln	Val	Ile	Met	Lys	Asn	Ile	Phe	Lys	Thr	Cys	Ala	Glu	Thr	Ala
				405					410					415	
Ala	Glu	Tyr	Gly	His	Glu	Asn	Asp	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala
			420					425					430		
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile	
		435					440					445			

<210> 83
 <211> 20
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gltA gene

 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n = inosine

 <400> 83
 aagatcacnt acatcgaygg 20

 <210> 84
 <211> 20
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gltA gene

 <400> 84
 tagaagtcta cgttcgggta 20

 <210> 85
 <211> 21
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gltA gene

 <400> 85
 gtcgacaata gcctgaatct g 21

 <210> 86
 <211> 21
 <212> DNA

 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 86

cggtggaacc ggtgctgaca t

21

<210> 87

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 87

gggtgggga attcggtcacg t

21

<210> 88

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 88

tgctcgtagcc gcggtagcgc a

21

<210> 89

<211> 1293

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(1290)

<400> 89

gtg gct tct gat aac aac aag gct gta ctg cac tac cct ggc ggc gaa 48

Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu

1 5 10 15

ttc gag atg ggc atc aag cag gcc acc gag ggt aac tcc ggt gtc atc 96

Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile

20 25 30

ctg ggt aag atg ctg tcg gaa acc ggt ctg gtc acc ttc gac ccc ggt 144

Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly

35 40 45

tat	gtc	agc	acc	ggt	tcc	acc	gaa	tcc	aag	atc	acc	tac	atc	gat	ggt	192
Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	Ile	Thr	Tyr	Ile	Asp	Gly	
	50					55					60					
gat	gca	ggc	atc	ctg	cgc	tac	cgc	ggc	tac	gac	att	gcg	gat	ctg	gcc	240
Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	Asp	Ile	Ala	Asp	Leu	Ala	
65					70					75					80	
gaa	aat	gcc	acc	ttc	aat	gag	gtc	tcc	tac	ctc	ctg	atc	aag	ggt	gag	288
Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	Leu	Leu	Ile	Lys	Gly	Glu	
				85					90					95		
ctc	ccg	acc	ccg	gaa	gag	ctc	cac	aag	ttc	aac	gac	gag	att	cgt	cac	336
Leu	Pro	Thr	Pro	Glu	Glu	Leu	His	Lys	Phe	Asn	Asp	Glu	Ile	Arg	His	
			100					105					110			
cac	acc	ctg	ctg	gac	gag	gac	ttc	aag	tcc	cag	ttc	aat	gtc	ttc	cct	384
His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	Gln	Phe	Asn	Val	Phe	Pro	
		115					120					125				
cgc	gat	gcc	cac	ccg	atg	gcc	acc	ctg	gcc	tcc	tcg	ggt	aac	atc	ctc	432
Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	Ser	Ser	Val	Asn	Ile	Leu	
	130					135					140					
tcc	acc	tac	tac	cag	gat	cag	ctg	gat	ccc	ctg	gat	gag	gct	cag	ctg	480
Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asp	Pro	Leu	Asp	Glu	Ala	Gln	Leu	
145				150					155						160	
gac	aag	gca	acc	gtc	cgc	ctg	atg	gcg	aag	gtt	ccg	atg	ctg	gct	gca	528
Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys	Val	Pro	Met	Leu	Ala	Ala	
				165					170					175		
tac	gca	cac	cgt	gcc	cgc	aag	ggt	gcg	ccg	tac	atg	tac	ccg	gac	aac	576
Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	Tyr	Met	Tyr	Pro	Asp	Asn	
			180					185					190			
tcc	ctc	aat	gcc	cgt	gag	aac	ttc	ctg	cgc	atg	atg	ttc	ggt	tac	ccg	624
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro	
		195					200					205				
acc	gag	ccg	tac	gag	gtt	gat	ccg	atc	atg	gtc	aaa	gcc	ctc	gac	aag	672
Thr	Glu	Pro	Tyr	Glu	Val	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys	
	210					215					220					
ctg	ctc	atc	ctg	cac	gca	gac	cac	gag	cag	aac	tgc	tcc	acc	tcc	act	720
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr	
225					230					235					240	
gtc	cgc	atg	atc	ggc	tcc	gcg	cag	gcg	aac	atg	ttc	gtc	tcc	atc	gcc	768
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala	
				245					250					255		
ggc	ggc	atc	aac	gca	ctc	tcc	ggc	ccg	ctg	cac	ggt	ggc	gcc	aac	cag	816
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln	
			260					265					270			
gct	gtc	ctc	gag	atg	ctc	gag	gag	atc	gca	gcc	aac	ggc	ggc	gac	gca	864
Ala	Val	Leu	Glu	Met	Leu	Glu	Glu	Ile	Ala	Ala	Asn	Gly	Gly	Asp	Ala	
		275					280					285				
acc	gac	ttc	atg	aac	cgc	gtg	aag	aac	aag	gag	aag	ggt	gtc	cgc	ctc	912
Thr	Asp	Phe	Met	Asn	Arg	Val	Lys	Asn	Lys	Glu	Lys	Gly	Val	Arg	Leu	
	290					295					300					
atg	ggc	ttc	gga	cac	cgc	gtc	tac	aag	aac	tac	gat	ccg	cgt	gca	gcc	960
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Ala	
305					310					315					320	

atc gtc aag gac acc gcc cac gag atc ctc gag cac ctc ggt ggc gac	1008
Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp	
325 330 335	
cca ctg ctg gat ctg gct ctc aag ctg gaa gaa atc gca ctc aac gac	1056
Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp	
340 345 350	
gat tac ttc atc tcc cgc aag ctg tac ccg aac gtg gac ttc tac acc	1104
Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr	
355 360 365	
ggc ctg atc tac cgc gcc atg ggc ttc ccg acg gac ttc ttc acc gtc	1152
Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val	
370 375 380	
ctg ttc gcc atc ggc cgc ctc ccg ggc tgg atc gcc cac tac cgc gag	1200
Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu	
385 390 395 400	
cag ctc gcc gat ccg ggc gcc aag atc aac cgt cct cgc cag atc tac	1248
Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr	
405 410 415	
acc ggt gag acc gca cgc aag atc atc ccc cgc gaa gag cgc tag	1293
Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg	
420 425 430	

<210> 90

<211> 430

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 90

Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu	
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Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile	
20 25 30	
Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly	
35 40 45	
Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly	
50 55 60	
Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala	
65 70 75 80	
Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu	
85 90 95	
Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His	
100 105 110	
His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro	
115 120 125	
Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu	
130 135 140	
Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu	
145 150 155 160	
Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala	
165 170 175	
Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn	

			180					185					190			
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro	
		195					200					205				
Thr	Glu	Pro	Tyr	Glu	Val	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys	
	210					215					220					
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr	
225					230					235					240	
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala	
			245						250					255		
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln	
			260					265					270			
Ala	Val	Leu	Glu	Met	Leu	Glu	Glu	Ile	Ala	Ala	Asn	Gly	Gly	Asp	Ala	
	275					280						285				
Thr	Asp	Phe	Met	Asn	Arg	Val	Lys	Asn	Lys	Glu	Lys	Gly	Val	Arg	Leu	
	290					295					300					
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Ala	
305					310					315					320	
Ile	Val	Lys	Asp	Thr	Ala	His	Glu	Ile	Leu	Glu	His	Leu	Gly	Gly	Asp	
			325					330						335		
Pro	Leu	Leu	Asp	Leu	Ala	Leu	Lys	Leu	Glu	Glu	Ile	Ala	Leu	Asn	Asp	
			340					345					350			
Asp	Tyr	Phe	Ile	Ser	Arg	Lys	Leu	Tyr	Pro	Asn	Val	Asp	Phe	Tyr	Thr	
	355					360						365				
Gly	Leu	Ile	Tyr	Arg	Ala	Met	Gly	Phe	Pro	Thr	Asp	Phe	Phe	Thr	Val	
	370				375						380					
Leu	Phe	Ala	Ile	Gly	Arg	Leu	Pro	Gly	Trp	Ile	Ala	His	Tyr	Arg	Glu	
385					390					395					400	
Gln	Leu	Ala	Asp	Pro	Gly	Ala	Lys	Ile	Asn	Arg	Pro	Arg	Gln	Ile	Tyr	
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Thr	Gly	Glu	Thr	Ala	Arg	Lys	Ile	Ile	Pro	Arg	Glu	Glu	Arg			
			420					425					430			

<210> 91
 <211> 1314
 <212> DNA
 <213> Brevibacterium lactofermentum

<220>
 <221> CDS
 <222> (1)..(1311)

<400> 91																
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Met	Phe	Glu	Arg	Asp	Ile	Val	Ala	Thr	Asp	Asn	Asn	Lys	Ala	Val	Leu	
1				5				10					15			
cac	tac	ccc	ggt	ggc	gag	ttc	gaa	atg	gac	atc	atc	gag	gct	tct	gag	96
His	Tyr	Pro	Gly	Gly	Glu	Phe	Glu	Met	Asp	Ile	Ile	Glu	Ala	Ser	Glu	
			20				25					30				
ggt	aac	aac	ggt	gtt	gtc	ctg	ggc	aag	atg	ctg	tct	gag	act	gga	ctg	144
Gly	Asn	Asn	Gly	Val	Val	Leu	Gly	Lys	Met	Leu	Ser	Glu	Thr	Gly	Leu	
		35				40						45				

atc	act	ttt	gac	cca	ggt	tat	gtg	agc	act	ggc	tcc	acc	gag	tcg	aag	192
Ile	Thr	Phe	Asp	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	
	50					55				60						
atc	acc	tac	atc	gat	ggc	gat	gcg	gga	atc	ctg	cgt	tac	cgc	ggc	tat	240
Ile	Thr	Tyr	Ile	Asp	Gly	Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	
65					70				75						80	
gac	atc	gct	gat	ctg	gct	gag	aat	gcc	acc	ttc	aac	gag	gtt	tct	tac	288
Asp	Ile	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	
				85					90					95		
cta	ctt	atc	aac	ggt	gaa	cta	cca	acc	cca	gat	gag	ctt	cac	aag	ttt	336
Leu	Leu	Ile	Asn	Gly	Glu	Leu	Pro	Thr	Pro	Asp	Glu	Leu	His	Lys	Phe	
			100					105					110			
aac	gac	gag	att	cgc	cac	cac	acc	ctt	ctg	gac	gag	gac	ttc	aag	tcc	384
Asn	Asp	Glu	Ile	Arg	His	His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	
		115					120					125				
cag	ttc	aac	gtg	ttc	cca	cgc	gac	gct	cac	cca	atg	gca	acc	ttg	gct	432
Gln	Phe	Asn	Val	Phe	Pro	Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	
	130					135					140					
tcc	tcg	gtt	aac	att	ttg	tct	acc	tac	tac	cag	gat	cag	ctg	aac	cca	480
Ser	Ser	Val	Asn	Ile	Leu	Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asn	Pro	
145					150					155					160	
ctc	gat	gag	gca	cag	ctt	gat	aag	gca	acc	gtt	cgc	ctc	atg	gca	aag	528
Leu	Asp	Glu	Ala	Gln	Leu	Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys	
				165					170					175		
gtt	cca	atg	ctg	gct	gcg	tac	gca	cac	cgc	gca	cgc	aag	ggc	gct	cct	576
Val	Pro	Met	Leu	Ala	Ala	Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	
			180					185					190			
tac	atg	tac	cca	gac	aac	tcc	ctc	aac	gcg	cgt	gag	aac	ttc	ctg	cgc	624
Tyr	Met	Tyr	Pro	Asp	Asn	Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	
		195					200					205				
atg	atg	ttc	ggt	tac	cca	acc	gag	cca	tac	gag	atc	gac	cca	atc	atg	672
Met	Met	Phe	Gly	Tyr	Pro	Thr	Glu	Pro	Tyr	Glu	Ile	Asp	Pro	Ile	Met	
		210				215					220					
gtc	aag	gct	ctg	gac	aag	ctg	ctc	atc	ctg	cac	gct	gac	cac	gag	cag	720
Val	Lys	Ala	Leu	Asp	Lys	Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	
225					230					235					240	
aac	tgc	tcc	acc	tcc	acc	gtt	cgt	atg	atc	ggc	tcc	gca	cag	gcc	aac	768
Asn	Cys	Ser	Thr	Ser	Thr	Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	
				245					250					255		
atg	ttt	gtc	tcc	atc	gct	ggc	ggc	atc	aac	gct	ctg	tcc	ggc	cca	ctg	816
Met	Phe	Val	Ser	Ile	Ala	Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	
			260					265					270			
cac	ggc	ggc	gca	aac	cag	gct	gtt	ctg	gag	atg	ctc	gaa	gac	atc	aag	864
His	Gly	Gly	Ala	Asn	Gln	Ala	Val	Leu	Glu	Met	Leu	Glu	Asp	Ile	Lys	
		275					280					285				
aac	aac	cac	ggc	ggc	gac	gca	acc	gcg	ttc	atg	aac	aag	gtc	aag	aac	912
Asn	Asn	His	Gly	Gly	Asp	Ala	Thr	Ala	Phe	Met	Asn	Lys	Val	Lys	Asn	
		290				295					300					
aag	gaa	gac	ggc	gtc	cgc	ctc	atg	ggc	ttc	gga	cac	cgc	gtt	tac	aag	960
Lys	Glu	Asp	Gly	Val	Arg	Leu	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	
305					310					315					320	

aac tac gat cca cgt gca gca atc gtc aag gag acc gca cac gag atc	1008
Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile	
325 330 335	
ctc gag cac ctc ggt ggc gac gat ctt ctg gat ctg gca atc aag ctg	1056
Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu	
340 345 350	
gaa gaa att gca ctg gct gat gat tac ttc atc tcc cgc aag ctc tac	1104
Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr	
355 360 365	
ccg aac gta gac ttc tac acc ggc ctg atc tac cgc gca atg ggc ttc	1152
Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe	
370 375 380	
cca act gac ttc ttc acc gta ttg ttc gca atc ggt cgt ctg cca gga	1200
Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly	
385 390 395 400	
tgg atc gct cac tac cgc gag cag ctc ggt gca gca ggc aac aag atc	1248
Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile	
405 410 415	
aac cgc cca cgc cag gtc tac acc ggc aag gaa tcc cgc aag ttg gtt	1296
Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val	
420 425 430	
cct cgc gag gag cgc taa	1314
Pro Arg Glu Glu Arg	
435	

<210> 92

<211> 437

<212> PRT

<213> Brevibacterium lactofermentum

<400> 92

Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu	
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His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu	
20 25 30	
Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu	
35 40 45	
Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys	
50 55 60	
Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr	
65 70 75 80	
Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr	
85 90 95	
Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe	
100 105 110	
Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser	
115 120 125	
Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala	
130 135 140	
Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro	
145 150 155 160	

Leu	Asp	Glu	Ala	Gln	Leu	Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys
				165					170					175	
Val	Pro	Met	Leu	Ala	Ala	Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro
			180					185					190		
Tyr	Met	Tyr	Pro	Asp	Asn	Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg
		195					200					205			
Met	Met	Phe	Gly	Tyr	Pro	Thr	Glu	Pro	Tyr	Glu	Ile	Asp	Pro	Ile	Met
		210				215					220				
Val	Lys	Ala	Leu	Asp	Lys	Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln
225					230					235					240
Asn	Cys	Ser	Thr	Ser	Thr	Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn
				245					250					255	
Met	Phe	Val	Ser	Ile	Ala	Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu
			260					265					270		
His	Gly	Gly	Ala	Asn	Gln	Ala	Val	Leu	Glu	Met	Leu	Glu	Asp	Ile	Lys
		275					280					285			
Asn	Asn	His	Gly	Gly	Asp	Ala	Thr	Ala	Phe	Met	Asn	Lys	Val	Lys	Asn
		290				295					300				
Lys	Glu	Asp	Gly	Val	Arg	Leu	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys
305					310					315					320
Asn	Tyr	Asp	Pro	Arg	Ala	Ala	Ile	Val	Lys	Glu	Thr	Ala	His	Glu	Ile
				325					330					335	
Leu	Glu	His	Leu	Gly	Gly	Asp	Asp	Leu	Leu	Asp	Leu	Ala	Ile	Lys	Leu
			340					345					350		
Glu	Glu	Ile	Ala	Leu	Ala	Asp	Asp	Tyr	Phe	Ile	Ser	Arg	Lys	Leu	Tyr
		355					360					365			
Pro	Asn	Val	Asp	Phe	Tyr	Thr	Gly	Leu	Ile	Tyr	Arg	Ala	Met	Gly	Phe
		370				375					380				
Pro	Thr	Asp	Phe	Phe	Thr	Val	Leu	Phe	Ala	Ile	Gly	Arg	Leu	Pro	Gly
385					390					395					400
Trp	Ile	Ala	His	Tyr	Arg	Glu	Gln	Leu	Gly	Ala	Ala	Gly	Asn	Lys	Ile
			405						410					415	
Asn	Arg	Pro	Arg	Gln	Val	Tyr	Thr	Gly	Lys	Glu	Ser	Arg	Lys	Leu	Val
			420					425					430		
Pro	Arg	Glu	Glu	Arg											
			435												

<210> 93

<211> 1656

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (309)..(1595)

<400> 93

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gccatccgcg	gaactgtgga	aggtccagtg	actgcttctt	gccaggttc	cattctgcaa	180
atgcacaaca	acgccaccat	catcgttgat	gaagcagcag	catccaagct	gaaaaatgct	240

gaccattacc gtctcatgga gcaattaaag ctgcgctaga aacaaaaagg aaagtactgt															300	
gtgggggct atg cac aca gaa ctt tcc agt ttg cgc cct gcg tac cat gtg															350	
Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val																
1 5 10																
act	cct	ccg	cag	ggc	aga	ctc	aat	gat	ccc	aat	gga	atg	tac	gtc	gat	398
Thr	Pro	Pro	Gln	Gly	Arg	Leu	Asn	Asp	Pro	Asn	Gly	Met	Tyr	Val	Asp	
15					20				25						30	
gga	gat	acc	ctc	cac	gtc	tac	tac	cag	cac	gat	cca	ggg	ttc	ccc	ttc	446
Gly	Asp	Thr	Leu	His	Val	Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	
				35				40						45		
gca	cca	aag	cg	acc	ggg	tgg	gct	cac	acc	acc	acg	ccg	ttg	acc	gga	494
Ala	Pro	Lys	Arg	Thr	Gly	Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	
			50				55						60			
ccg	cag	cga	ttg	cag	tgg	acg	cac	ctg	ccc	gat	gct	ctt	tac	ccg	gat	542
Pro	Gln	Arg	Leu	Gln	Trp	Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	
		65				70						75				
gta	tcc	tat	gac	ctg	gat	gga	tgc	tat	tcc	ggc	gga	gcc	gta	ttt	tct	590
Val	Ser	Tyr	Asp	Leu	Asp	Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Ser	
	80					85					90					
gac	ggc	acg	ctt	aaa	ctt	ttc	tac	acc	ggc	aac	cga	aaa	att	gac	ggc	638
Asp	Gly	Thr	Leu	Lys	Leu	Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	
	95				100					105					110	
aag	cg	cg	gcc	acc	caa	aac	ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	686
Lys	Arg	Arg	Ala	Thr	Gln	Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	
				115					120					125		
ctg	atg	ggc	ggc	att	cat	cg	cg	tcg	cct	aaa	aat	ccg	ctt	atc	gac	734
Leu	Met	Gly	Gly	Ile	His	Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	
			130					135					140			
gga	ccc	gcc	agc	ggg	ttt	acg	ccc	cac	tac	cg	gat	ccc	atg	atc	agc	782
Gly	Pro	Ala	Ser	Gly	Phe	Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	
		145					150					155				
cct	gat	ggg	gat	ggg	tgg	aag	atg	gtt	ctt	ggg	gct	cag	cg	gaa	aac	830
Pro	Asp	Gly	Asp	Gly	Trp	Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	
	160					165					170					
ctc	acc	ggg	gca	gcg	gtt	cta	tac	cg	tcg	gca	gat	ctt	gaa	aac	tgg	878
Leu	Thr	Gly	Ala	Ala	Val	Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	
					180					185					190	
gaa	ttc	tcc	ggg	gaa	atc	acc	ttt	gac	ctc	agc	gac	gca	caa	cct	ggg	926
Glu	Phe	Ser	Gly	Glu	Ile	Thr	Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	
				195					200					205		
tct	gcc	cct	gat	ctc	gtt	cct	ggc	ggc	tac	atg	tgg	gaa	tgc	ccc	aac	974
Ser	Ala	Pro	Asp	Leu	Val	Pro	Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	
			210					215					220			
ctt	ttt	acg	ctt	cg	gat	gaa	aaa	acc	ggc	gaa	gac	ctc	gat	gtg	ctg	1022
Leu	Phe	Thr	Leu	Arg	Asp	Glu	Lys	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	
		225					230					235				
att	ttc	tgt	cca	caa	gga	ttg	gac	cgt	atc	gat	gat	gag	gtt	act	cac	1070
Ile	Phe	Cys	Pro	Gln	Gly	Leu	Asp	Arg	Ile	Asp	Asp	Glu	Val	Thr	His	
	240					245					250					
tac	gca	agc	tct	gac	cag	tgc	gga	tat	gtc	gtc	ggc	aag	ctt	gaa	gaa	1118
Tyr	Ala	Ser	Ser	Asp	Gln	Cys	Gly	Tyr	Val	Val	Gly	Lys	Leu	Glu	Glu	

255		260		265		270	
acg acc ttc cgt gtc	ctg cga gga ttc agc	gag ctg gat ttc ggt	cat	1166			
Thr Thr Phe Arg Val	Leu Arg Gly Phe Ser	Glu Leu Asp Phe Gly	His				
	275	280	285				
gaa ttc tac gcg ccg	cag gtt gca gtc aac	ggt tcc gat gcc tgg	ctt	1214			
Glu Phe Tyr Ala Pro	Gln Val Ala Val Asn	Gly Ser Asp Ala Trp	Leu				
	290	295	300				
gtg ggc tgg atg gga	ttg cct gca cag gat	gat cac cca aca gtt	gcg	1262			
Val Gly Trp Met Gly	Leu Pro Ala Gln Asp	Asp His Pro Thr Val	Ala				
	305	310	315				
cag gaa gga tgg gtg	cac tgc ctg acc gtt	cct cgc agg ctt cat	ttg	1310			
Gln Glu Gly Trp Val	His Cys Leu Thr Val	Pro Arg Arg Leu His	Leu				
	320	325	330				
cgt aac cat gcg atc	tat caa gag ctt ctt	ctc cca gaa ggg gag	tcg	1358			
Arg Asn His Ala Ile	Tyr Gln Glu Leu Leu	Leu Pro Glu Gly Glu	Ser				
	335	340	345	350			
ggg gta act aga tct	gta tta ggt tct gaa	cct gtc cga gta gac	atc	1406			
Gly Val Thr Arg Ser	Val Leu Gly Ser Glu	Pro Val Arg Val Asp	Ile				
	355	360	365				
cga gac aat gtt tcc	ctc gag tgg gat ggt	gtc cgg ttg tct gtg	gat	1454			
Arg Asp Asn Val Ser	Leu Glu Trp Asp Gly	Val Arg Leu Ser Val	Asp				
	370	375	380				
cgc gat ggc gat cgt	cgt gta gct gaa gta	aaa cct ggc gaa tta	gtg	1502			
Arg Asp Gly Asp Arg	Arg Val Ala Glu Val	Lys Pro Gly Glu Leu	Val				
	385	390	395				
atc gcg gac gat aat	aca gcg att gag ata	aca gca ggt cat ggc	cag	1550			
Ile Ala Asp Asp Asn	Thr Ala Ile Glu Ile	Thr Ala Gly His Gly	Gln				
	400	405	410				
gtt tcc ttc gct ttc	cgc acc ttc aaa ggt	gac act att gag aga		1595			
Val Ser Phe Ala Phe	Arg Thr Phe Lys Gly	Asp Thr Ile Glu Arg					
	415	420	425				
taagtcataa aaaagggcct tctgtggcgg attgtacaaa tacttcgcaa aatcccttga				1655			
t				1656			

<210> 94

<211> 429

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 94

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro	
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Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp	
20 25 30	
Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro	
35 40 45	
Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln	
50 55 60	
Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser	
65 70 75 80	
Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly	

				85					90					95		
Thr	Leu	Lys	Leu	Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	Lys	Arg	
			100					105					110			
Arg	Ala	Thr	Gln	Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	
		115					120					125				
Gly	Gly	Ile	His	Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	
	130					135					140					
Ala	Ser	Gly	Phe	Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	
145					150					155					160	
Gly	Asp	Gly	Trp	Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	
				165					170					175		
Gly	Ala	Ala	Val	Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	
			180					185					190			
Ser	Gly	Glu	Ile	Thr	Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	
	195						200					205				
Pro	Asp	Leu	Val	Pro	Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	
	210					215					220					
Thr	Leu	Arg	Asp	Glu	Lys	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	
225					230					235					240	
Cys	Pro	Gln	Gly	Leu	Asp	Arg	Ile	Asp	Asp	Glu	Val	Thr	His	Tyr	Ala	
				245					250					255		
Ser	Ser	Asp	Gln	Cys	Gly	Tyr	Val	Val	Gly	Lys	Leu	Glu	Glu	Thr	Thr	
			260					265					270			
Phe	Arg	Val	Leu	Arg	Gly	Phe	Ser	Glu	Leu	Asp	Phe	Gly	His	Glu	Phe	
		275					280					285				
Tyr	Ala	Pro	Gln	Val	Ala	Val	Asn	Gly	Ser	Asp	Ala	Trp	Leu	Val	Gly	
	290					295					300					
Trp	Met	Gly	Leu	Pro	Ala	Gln	Asp	Asp	His	Pro	Thr	Val	Ala	Gln	Glu	
305					310					315					320	
Gly	Trp	Val	His	Cys	Leu	Thr	Val	Pro	Arg	Arg	Leu	His	Leu	Arg	Asn	
				325					330					335		
His	Ala	Ile	Tyr	Gln	Glu	Leu	Leu	Leu	Pro	Glu	Gly	Glu	Ser	Gly	Val	
			340					345					350			
Thr	Arg	Ser	Val	Leu	Gly	Ser	Glu	Pro	Val	Arg	Val	Asp	Ile	Arg	Asp	
		355					360					365				
Asn	Val	Ser	Leu	Glu	Trp	Asp	Gly	Val	Arg	Leu	Ser	Val	Asp	Arg	Asp	
	370					375					380					
Gly	Asp	Arg	Arg	Val	Ala	Glu	Val	Lys	Pro	Gly	Glu	Leu	Val	Ile	Ala	
385					390					395					400	
Asp	Asp	Asn	Thr	Ala	Ile	Glu	Ile	Thr	Ala	Gly	His	Gly	Gln	Val	Ser	
				405					410					415		
Phe	Ala	Phe	Arg	Thr	Phe	Lys	Gly	Asp	Thr	Ile	Glu	Arg				
			420					425								

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying scrB gene

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gtacatattg tcgtagaac gcgtaatacg actca

35

<210> 96

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying scrB gene

<400> 96

cgtagaacg cgtaatacga ctactatag ggaga

35

<210> 97

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
LA cloning of scrB

<400> 97

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<210> 98

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
LA cloning of scrB

<400> 98

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<210> 99

<211> 30

<212> DNA

<213> Artificial Sequence

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<210> 100
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<400> 100
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<210> 101
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<400> 101
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<210> 102
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<210> 103
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<400> 103
 gaagatctct atgaccagcg catcaagctg 30

<210> 104
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<400> 104
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<210> 105
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<210> 106
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 gcgcctgcag gcaccaggat gccctcaacc ag 32

<210> 107
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<213> Artificial Sequence

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ggggtaccga tcactataac cccacagcac

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<210> 108

<211> 30

<212> DNA

<213> Artificial Sequence

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amplifying gltA gene

<400> 108

ggggtaccct ggctgatctg aactaggcgc

30